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AGENCOURT	UI-R-EPO-	DG2-93n7	K-EST0196	UI-R-DY1-	AGENCOURT	0009b06.x	BY755449	UI-R-FSO-	387409 MA	DKFZp686E	AGENCOURT	602311010	N112 SSH-	602268114	UI-E-EJ0-	EST6973 h	UI-E-EJ0-	BX103101	HTM1-183F	599432 MA	AGENCOURT	603194629

RESULT 1 AY403218 LOCUS DEFINITION Homo sapiens STEAP gene, genomic survey sequence. AY403218 AY403218.1 GI:39759201 AY403218 1050 bp DNA linear GSS 15-DEC VIRTUAL TRANSCRIPT, partial sequence, GSS 15-DEC-2003

ALIGNMENTS

sapiens (human)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE TITLE AUTHORS Hominidae; Homo.

(bases 1 to 1050)

(clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Lu, F., Murphy, B., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens

gene trios Science 302 (5652), 1960-1963 (2003) 4671302

JOURNAL
PUBMED
REFERENCE
AUTHORS COMMENT JOURNAL TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers 2 (bases 1 to 1050)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M. Direct Submission

ORIGIN FEATURES source /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /gene="STEAP" /locus_tag="HCM1484" .1050

Query Match 87.7%; Best Local Similarity 99.9%; Matches 1049; Conservative Score 1048.4; DB 10; Length 1050; Pred. No. 2.1e-232; 0; Mismatches 1; Indels 0; Gaps

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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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This sequence was made by sequencing genthem based on alignment.
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Hominidae; Homo.

E 1 (bases 1 to 884)

S NIH MGC http://mgc.nci.nih.gov/.

S NIH MGC http://mgc.nci.nih.gov/.

S National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

C Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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/clone_lib="MAPCL"
/clone_lib="MAPCL"
/clone_lib="MAPCL"
/note="Wetctor: pcWV-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Wetctor: pcWV-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Wetctor: pcWV-SPORT6; Site_1: Language and muscle."
// Subtracted with brain, liver, lung, kidney and muscle.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6719746"
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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H. Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
                                                                                                                                                                                                               Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1211)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Please visit our web site (http://genome.gsc.riken.jp/)
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                                                                                                                                                 GTCATGGAGATCAGTGACGATGTTACAAACCCAGAACAACTTTGGAAAAATGAAGCCAAAG
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       AGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCA
                                                      GGAAACCTGGAAGATGACAGTTACTCGACTAAGGACTCGGGAGAGACGAGCATGCTGAAA
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/strain="C57BL/6J"
/db_xref="FANTOM_D8:2410007B19"
/db_xref="taxon:10090"
/clone="2410007B19"
/cell type="ES cells"
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/prottain_id="BAB26938.1"
/db_xref="gfi:12845881"
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/translation="MEISDDVINPEQLWKMKPKGNLEDDSYSTKDSGETSMLKRPGLS
/translation="MEISDDVINPEQLWKMKPKGNLEDDSYSTLLREITYPLATSR
EQYFYKI:PILVINVIENVALTYLLATYLPGELAAVVQLRNGTKYKKFPPWLDRWMLA
KKQFGLLS=FFAVLHAVYSLSYPWLRSYRYKLLNWAYKQVQQNKEDAWVEHDVWRMEL
KKQFGLLS=FFAVLHAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTVHALVFAWNK
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1 (bases 1 to 1050)

1 (bases 1 to 1050)

1 (clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Petriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                  TTGCCAGGAGAGTTAGCGGCAGTTGTACAGCTTCGCAATGGAACCAAGTACAAGAAGTTC
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/locus_tag="HCM1484"
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18 (bases 1 to 720)

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18 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

18 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

18 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

19 Tumor Gene Index

10 Unpublished (1997)

11 Unpublished (1997)

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTTTTGCCTGGAATAAATGGGTAGATGTCAGTCAATTTGTATGGTACATGCCTCCGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTGTATGGTATACACCTCCAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACTATATTCAGAGCAAGCTAGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCTCTTGGCTGACATCTATTCCATCTGTGAGCGACTCTTTAACCTGGAGAGAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATGATGTCTGGAGAATGGAGATTTATGTGTCCCTGGGGATTGTGGGGGCTGGCCATCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATGATGTTTGGAGAATGGAGATTTATGTGTCTCTCTGGGAATTGTGGGATTGGCAATACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCTACTCAACTGGGCTTACAAACAGGTTCAACAAAACAAAGAGGATGCCTGGGTAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATT 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTATGATAGCTGTTTTCCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCCTG 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACTATATTCAGAGCAAACTAGGAATTGTCTCTCTTCTTCTGGGCACAGTACACGCTTTG
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                                                                                                                                                primer: M13 FORWARD
/organism="Homo sapiens"
/mol_type="mRNA"
                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (human)
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CCAGTTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCA

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Best Local Similarity
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                                                                                                                                                                                                                                     GATAGATATAAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCT
                                                                                                                                                                                                                                                                       GATAGATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCT
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CCAGTTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTATCACCA 1135
                                                                                                                                                 TCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAT 181
                                                                                                                                                                                   TCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAT 1015
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// clone lib="NOI] CGAP ED1"

// note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
// note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI CGAP ED1 is a normalized GDNA library
containing the following tissue(s): Chondrosarcoma cell
line CS5. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
CDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT).8 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_TISSUE=chondrosarcoma
TAG_LB=UI-H=BD1
TAG_SEQ=CGTCAAGGCT"
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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
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/clone="UI-H-ED1-axr-o-23-0-UI"
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SOURCE
ORGANISM
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VERSION
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TITLE
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Best Local Similarity
Matches 786; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1549 row: b column: 05
High quality sequence stop: 704.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ggapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, I
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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1 (bases 1 to 881)
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BG565247
BG565247.1 GI:13572900
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881 bp mRNA linear EST 10-APR-2001
602582917F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4710436 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
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                       CATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCA
                                                                                                     TCAACAATATTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTC
                                                                                                                                                            ATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCA
                                                                                                                                                                                                  ATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:4710436"
//clone_lib="NIH_MGC_76"
/clone_lib="NIH_MGC_76"
/clone_lib="NIH_MGC_76"
/clone_lib="NIH_MGC_76"
/clone_lib="NIH_MGC_76"
/clone_lib="NIH_MGC_76"
/clone_lib="NIH_MGC_76"
/clone_lib="NIH_MGC_76"
/clone="Contains as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACAGGCGGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                              58.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                              Score 692.8; DB 2; Pred. No. 7.2e-150;
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REFERENCE AUTHORS TITLE SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 8 BG762026 COMMENT DEFINITION Pocus Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can Hominidae; Homo.

1 (bases 1 to 961)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian
Unpublished (1999)

Contact: Robert Strausberg, Ph.D. found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLCM1713 row: h column: 21 Plate: LLCM1713 row: h column: 21 High quality sequence stop: 750. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens BG762026.1 mRNA sequence. BG762026 BG762026 961 bp n 602718984F1 NIH_MGC_49 Homo Bapiens GI:14072679 cDNA clone IMAGE: 4858820 5', Gene linear Collection EST 15-MAY-2001 ğ

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                         AGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAAT--GGAGAT
                                                                    CTCTGTCTTACGCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
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AGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTCGGAGAATGCGCCACT
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_49"
/clone_lib="NIH_MGC_49"
/clone_lib="NIH_MGC_49"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
/cori; cDNA made by oligo-dT priming. DIrectionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library. |"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Unpublished (2002)
Contact: DNA Core Facility (Bovine
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Prather, R.S., Antoniou, E., Garverick, H.A., Roberts, R.M., Smith, M.F. and Youngquist, R. Subandarant NRI-2002-03476: Bovine ESTs: For
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CV983083.1 GI:56143804
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Fax: (573)884-5552
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
/mol type="mRNA"
/db_xref="taxon:9913"
/dev_stage="Conceptus-Cc
                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.circlearanch.com/home.html). These heifers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples consisted of the following: germinal vesicle-stage occytes; in vitro derived embryos (2-cell, morula, blastocyst and nuclear transfer blastocyst; in vivo blastocyst and conceptuses (days 8, 14, 16 and 18); corpora lutes (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early
http://genome.rnet.missouri.edu/Bovine/Methods.html.
Library construction (Standard Protocol): All procedures
have been described in detail elsewhere (Soares et al.,
1994; Bonaldo et al., 1996; Jiang et al., 2001). Total
cellular RNA from each sample was isolated by using
STAT-60 reagent (Tel-Test, Friendswood, TX) and the
poly(A)+ RNA was obtained by two rounds of purification
with the Oligotex mRNA isolation kit (Qiagen) according t
the manufacturer's instructions. The libraries were
constructed essentially as described by the manufacturer'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=Tvector: pSport1; Funding: The production of ESTs submitted in this project was funded by USDA Grant MRI-2002-03476 entitled 'Bovine ESTS: Focus on Female Reproduction' to RS Prather(Primary Investigator), E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, Smith and RS Youngquist. Genetic Source: Heifers for the project were purchased from Circle A Ranch, Iberia, MO
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                                                                                                                                                                                                                                                                              selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (mega-library) for more extensive sequencing.
Bioinformatics work was performed by GK Springer's bioinformatics group in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovine@rnet.missouri.edu. Citations: Bonaldo MF, Lennon G, Soares MB, Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotens MB, MF and Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAG_TISSUE=Conceptus-Corpus Luteum (mixed)
TAG_SEQ=Not found"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyre Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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       DN997716

697 bp mRNA linear EST 17-MAY-2005
TC115356 Human breast cancer tissue, large insert, pCMV expression
library Homo sapiens cDNA clone TC115356 5' similar to Homo sapiens
six transmembrane epithelial antigen of the prostate 1 (STEAP1),
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/tissue_types"large_cell_carcinoma, undifferentiated"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 69"
/clone_Torgan: lung, Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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1 (bases 1 to 697)

Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M., Zhang, X., Jay, G. and He, W.

High-throughput cloning of full-length human cDNAs directly from the contact of the contact of the contact of the contact Kovacs, KF

High Throughput cDNA Cloning
OriGene Technologies, Inc. ( www.origene.com )

6 Taft Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606
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Technologies Inc.
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Please contact OriGene for access.
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Seq primer: pCMV6 5prime forward
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                                        CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG
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CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG
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(note="Organ: Mammary gland (cancer tissue); Vector: prove-torgan: Mammary gland (cancer tissue); Vector: prove-torgan: Mammary gland (cancer tissue); Vector: prove-torgan: Site 2: Xhol/Sall compatible ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected fend sequence verification of full-length genes"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TC115356"
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/clone_Tib="Human breast cancer tissue,
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Tissue Procurement: NCI
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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/tissue_type="mixed (pool of 40 RNAs)"
/lab host="PH10B (T1-phage-resistant)"
/clome_libe="NIH_MGC_142"
/clome_libe="NIH_MGC_142"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccatt
                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6496341"
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  CX757709 742 bp n
AGENCOURT 41384224 NIH MGC 278 Homo
IMAGE:7772991 3', mRNA sequence.
CX757709
CX757709.1 GI:58054365
EST.
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ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'-AACCAGTGGTATCAACGCAGAGTGGCCATTACGCCGG-3' and 5'-ATTCTAGAGGCCGAGGCGGCGAAGTGGCCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >0.5 size fraction (other fractions present in NIH_MGC 141). Library created in the laboratory of M. Brownstein (NIMH NIH). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                    4.3%, salivary
3' adaptors wer
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Similarity
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                                                                                     GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACT-GGGCATATCAA
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mRNA linear EST sapiens cDNA clone

24-JAN-2005

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National Institutes of Health, Mammalian Ge
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Meri Firpo
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                           GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCCAGCATGCTAA 180
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AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT
                                                                                                                                                                                                                                                                 CTGAGACTCACGGTCAAGCTACGGCGAGGAGTGGGTGGCTGAAGCCATACTATTTTATAG
                                                                  quality sequence start: 6 quality sequence stop: 726.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Togan: Blastocyst; Vector: pExpress-1; Site_1: EcoRV; Site_2: Not!; RNA obtained from pluripotent cell line derived from blastocyst inner cell mass (cell line HSF-1.14, NIH Registry designation UC01. Positive for OCT4 expression by rtPCR, positive for SSEA-3, SSEA-4, expression by rtPCR, positive for SSEA-3, SSEA-4, expression by rtPCR, positive for SSEA-3, SSEA-1, lat, inmunofluorescence. Negative for SSEA-1 by immunofluorescence. Negative for SSEA-1 by immunofluorescence. Passage 35. This line is a subclone of the parental line; the parental line was subcloned to remove aneuploid cells). cDNA was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5'-pGACTAGTTCTAGAGCGGCCGCCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25 kb resulted in an average insert size of 1.9 kb. This primary library is non-normalized (normalized primary library is NIH MGC 279) and was constructed by Express Genomics (Frederick, MD). Note: this is a Mammalian Gene collection library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="pluripotent cell line
blastocyst inner cell mass"
/lab_host="DH10B TonA"
/clone_lib="NIH_MGC_278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              using oligo-dT primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7772991"
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Pred. No. 2.2e-141;
0; Mismatches 18;
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                                                                                                                                                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh.
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                      Hominidae; Homo.

1 (bases 1 to 783)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian

Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI552907.1 GI:15440219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                         Plate: LLAM11700 row: e column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAACTTCCCATCAACAATATTTTTATAAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cagaactrcagcacacacaggaactctrtccacagtggcactrgccaattaaaatagctg
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                                                                                                                                                                  quality sequence stop: 769.
Location/Qualifiers
                                             /organism="Homo sapiens"
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/clone="rMAGE:527295"
/tissue_type="hippocampus"
/lab_host;"DH108"
/clone lib="NIH MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  783 bp
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ORIGIN

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RESULT 15
CX753134
LOCUS
DEFINITION
                          ACCESSION
VERSION
KEYWORDS
  ORGANISM
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                                                      CX753134 825 bp m AGENCOURT 40991781 NIH MGC 281 Homo IMAGE:7780881 3', mRNA sequence.
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    Homo
                                         CX753134.1 GI:58049789
                                                                                                                                                                                                 ACAGGTCCAACAAAATAAAGAAGATGC 685
                                                                                                                                                                                                                                                                                                   TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCA-TGCAATTTAT
                                                                                                                                                                                                                                                                                                                                                           CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG
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 sapiens
sapiens
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Pred. No. 4.2e-141;
D; Mismatches 5;
                                                                                 sapiens cDNA clone
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Matches 671
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CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG
                                                     CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG
                          CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG
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SOURCE

360

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CDNA Library Preparation: Express Genomics CDNA Library Arrayed by: The I.M.A.G.R. Consortium (LLNL) DNA Sequencing by: Agencourt Bloscience Corporation Clone distribution: MGC clone distribution information car found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov row: a column: 07 High quality sequence stop: 538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Meri Firpo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 825)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGAACTGCCCTT
                                                                                                                    GAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA
                                                                                                                                                                                                  AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA
                                                                                                                                                                                                                                           AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAAATGAAGCCTA
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                                                                                 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA
                                                                                                                                                                                                                                                                                                                         CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Clone_lib="NIH MGC_281"
//Clone_lib="NIH MGC_281"
//Clone_"Organ: Blastcoyst; Vector: pExpress-1; Site_1:
ECORV; Site_2: Not1; RNA obtained from pluripotent_cell
line derived from blastcoyst inner cell mass (cell line
HSF-6, NIH Registry designation UCO6. Positive for OCT4
expression by rtPCR, positive for SSEA-3, SSEA-4,
Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
SSEA-1 by immunofluorescence Passage 62. cDNA was primed
using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCGAGCGCCCCC(T)25-3' and cloned into
the ECORV/NotI sites of pExpress-1. Size-selection >1.25
kb resulted in an average insert size of 2.0 kb. This
primary library is normalized (non-normalized primary
library is NIH MGC_280) and was constructed by Express
Genomics (Frederick, MD). Note: this is a Mammalian Gene
Collection library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="pluripotent cell line
blastocyst inner cell mass"
/lab_host="DH108 TonA"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 5.2e-141;
0; Mismatches 9;
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Search completed: December 5, 2005, 03:12:12 Job time : 5464.54 secs

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Listing first 45 summaries
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ARBSULT 1 ARAB93924 ID AAHS XX AC AAHS AC CYCC AC AAHS AC AA AA AAN AC WO200151633-A2 Homo sapiens. Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis; ss. P789P full length cDNA sequence. 04-OCT-2001 AAH93924 standard; cDNA; 1195 BP. AAH93924; (first entry)

ALIGNMENTS

19-JUL-2001.

16-JAN-2001; 2001WO-US001574.

14-JAN-2000; 2000US-00483672

(CORI-) CORIXA CORP.

Xu J, Dillon DC, Mit Kalos MD, Fanger GR, Wang A, Meagher MJ; Mitcham GR, Day Ή̈́Ę Harlocker SL, Jiang Y, Reed SG; Retter MW, Stolk JA, Skeiky YAW

WPI; 2001-425873/45.

New polynucleotide encoding a prostate-specific protein, monitoring and treating prostate cancer in a patient and for diagnosing, use in

Claim 1; Page 510; 543pp; English.

The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and

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Best Local Simi
Matches 1195;
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                                             CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA
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09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
99-AUG-2000;
29-AUG-2000;
06-SEP-2000;
06-CT-2000;
01-OCT-2000;
10-OCT-2000;
                                                                                                                                                                                                                                                                             Fanger
Li SX,
The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) as
                                                                                          Claim
                                                                                                                                                                                                           WPI; 2001-639232/73.
P-PSDB; AAU69927.
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                                                                                                                                        human prostate-specific polypeptides and polynucleotides useful diagnosis and treatment of cancer, especially prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                      CORIXA CORP.
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  CAATGGTTTCCATCACTCTTGGCATTGGTTTTACCTGCCAGGTGTGATAGCAGCAATTG
                                                                                                                                                                                                                                                                                                  CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC
                                                                                                                                                                                                                                                                                                                                                                                   CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG
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                                                                                     CAATGGTTTCCATCACTCTTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG
                                                                                                                                                                                                                                                                      CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC
                                                                                                                                                                                                                                                                                                                                                            CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG
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Pred. No. 4.
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Carter D;
Hural J;
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01-AUG-1997;
10-FEB-1998;
25-FEB-1998;
14-JUL-1998;
23-SEP-1999;
15-JAN-1999;
09-APR-1999;
13-JUL-1999;
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herapy; gene; ss.
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99US-00232149.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; vaccine; cytostatic; immunostimulant;
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Best Local Similarity
Matches 1195; Conserv
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17-JAN-2000
27-MAR-2000
09-MAY-2000
112-MAY-2000
113-JUN-2000
27-JUN-2000
27-JUN-2000
29-AUG-2000
06-SEP-2000
06-SEP-2000
10-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                               The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatmet of cancers, particularly prostate cancer. The present sequence is a cl described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New prostate-specific polynucleotides for diseases, in particular prostate cancer, a progression of cancer.
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Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick '
Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson I
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MITCHAM J L.
HARLOCKER S L.
JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HEPLER W T.
CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG
                                                       CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG
                                                                                                                                 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 878;
                                                                                                                 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGAGCCAGCATGCTAA
                                                                                                                                                                                                                                                                                             Conservative
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2000US-00577379.

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2000US-00636215.

2000US-00657236.

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Pred. No. 4.4e-276;
Mismatches 0;
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                                                                             CAACTTCCCATCAACAATATTTTATAAAAATTCCAATCCTGGTCATCAACAACAAGTCTTGC
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ABK92128;
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            DNA;
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Prostate cancer-associated DNA sequence #14

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prostate tumour tissue; human; mammal;

cytostatic;

cancer;

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cc associated transcript in a cell from a patient. The method comprises
cc contacting a biological sample from the patient with prostate cancer-
cc associated polynuclectides (designated PC genns) that selectively
cc hybridise to a sequence that is at least 80% identical to them. The
cc hybridise to a sequence that is at least 80% identical to them. The
cc prostate cancer-associated polynuclectide sequences are differentially
cc expressed in prostate tumour tissue or in prostate cancer and are derived
cc from the tissues of various organisms such as humans or other mammals
cc (e.g. mice, sheep and dogs). The methods of the invention are useful for
cd disgnosing and treating prostate cancer in mammals. The prostate cancer.
cc associated genes are useful for diagnosing or treating prostate cancer.
cc as well as for identifying modulators of prostate cancer or agents that
cc inhibit prostate cancer. The nucleic acid sequences are particularly
cc useful in gene therapy, as a vaccine or in antisense applications.
cc ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
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Best Local Similarity 100
Matches 1195; Conservative
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08-DEC-2000;
08-DEC-2000;
08-DEC-2001;
16-MAR-2001;
16-MAR-2001;
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24-APR-2001;
30-APR-2001;
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                                                           GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA
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AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT
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Matches 1195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New prostate-specific proteins and genes, useful in gene therapy, particularly for stimulating an immune response in a patient, or treating prostate cancer in a patient, as well as for diagnosing prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson
Kalos MD, Fanger RR, Retter MW, Stook JA, Day CH, Vedvick TS;
Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
Mcneill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAY-2001; 2001US-00852911.
29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
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                                                                                                                                                                                                                                                                                                                                                                                     illustrate the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer.

Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in ADB75177-ADB75631 represent marker CDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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22-AUG-2001; 2001US-0314356P.
25-SEP-2001; 2001US-0325020P.
12-DEC-2001; 2001US-0341746P.
05-MAR-2002; 2002US-0362158P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1195 BP; 382 A; 221 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with
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CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG
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Human; ss; prostate specific cDNA; cytostatic; immunostimulant; gene therapy; cell therapy; vaccine; T-cell epitope; class I major histocompatibility complex allele; MHC; prostate tumour; antigen presenting cell. prostate cancer;

Homo sapiens US2003185830-A1

12-NOV-2002; 2002US-00294025

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The invention relates to an isolated polypeptide comprising no more than CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The CC peptides comprise a fragment ADB13563 of that contain naturally processed CC T-cell epitopes for 3 class I major histocompatibility complex (MIC) CC cDNA, one of 648 disclosed as new. Also included are nucleic acids cencoding the proteins and peptides, expression vectors, a host cell transformed with the vector, an isolated antibody (or antigen binding CC fragment) that specifically binds to the protein or peptide, detecting the presence of a cancer in a patient (comprising contacting a patient CC sample with a binding agent that binds to the peptides or a polypeptide coff reagment and comparing the amount of polypeptide that binds to the agent and comparing the amount of polypeptide that binds to the agent and comparing the presence of cancer), a fusion protein comprising the peptides or proteins, stimulating or expanding T cells specific for a tumour protein comprising contacting T cells with the peptides or the isolated T cell population, treating prostate cancer in a patient and treating prostate cancer in a patient comprising contacting the peptides, nucleic acids, antibodies or compounds, determining the presence of a cancer in a patient with the peptides or antigen presenting cells that express (the peptides so that the T cells proliferate, and administering the peptides (or an oligonucleotide that hybridises to nucleic acid encoding them), is used to detect the concilean presenting cells to the patient. The peptides (or an oligonucleotide, or anciden presenting colls expressing the nucleic acid, are used to concer in a patient comprising the peptides, or an oligonucleotide, or anciden acids, antibodies, fusion proteins, T cell populations or antigen concerns.
         25-FEB-1998
14-JUL-1998
23-SEP-1998
15-JAN-1999
09-AFR-1999
13-JUL-1999
11-NOV-1999
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01-AUG-1997;
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39 98US-00159812
39 99US-00232149
39 99US-00288946
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2001US-00012896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              presenting cells are used to stimulate an immune response or treat prostate cancer in a patient. The present sequence is a known cDNA showing sequence similarity to one of the disclosed human prostate specific cDNAs. Note: Except where otherwise indicated, the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1195 BP;
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TIGITTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG
                                                       CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA
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                                                                                                                               ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC
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                       Query Match
Best Local Sim
Matches 1195;
                                                                                           The present invention relates to a method of prognosticating metastasis in a breast cancer patient involves identifying differential modulation of each gene relative to the expression of the same genes in a normal population in combination of genes. The invention is useful for prognosticating breast cancer in a patient. The present sequence is huma STEAP (six transmembrane epithelial antigen of the prostate) DNA used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human STEAP
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                                                                                                                                                                                                                            prognosticating metastasis in a breast cancer patient comprises identifying differential modulation of each gene relative to the expression of the same genes in a normal population in combination
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                                                                       Sequence 1195
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                                    Similarity
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  CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (six transmembrane epithelial antigen of the prostate) DNA.
                        Conservative
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ane epithelial antigen of the prostate; ds.
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Pred. No. 4.4e-276;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosing cancer comprises identifying differential modulation gene (relative to the expression of the same genes in a normal population) in a combination of genes.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                             standard;
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25-FEB-1997; 97US-00806099.
01-AUG-1997; 97US-0020956.
25-FEB-1998; 98US-00020956.
25-FEB-1998; 98US-0015453.
23-SEP-1998; 98US-00159812.
15-JAN-1999; 99US-00232149.
09-APR-1999; 99US-00232149.
109-APR-1999; 99US-00443686.
13-JUL-1999; 99US-00443686.
14-JAN-2000; 2000US-00433772.
27-MAR-2000; 2000US-00536857.
19-MAY-2000; 2000US-00536857.
19-MAY-2000; 2000US-00568100.
12-MAY-2000; 2000US-0059793.
27-JUN-2000; 2000US-0059793.
27-JUN-2000; 2000US-0055729.
09-AUG-2000; 2000US-0065723.
09-AUG-2000; 2000US-0065723.
09-AUG-2000; 2000US-0065723.
10-OCT-2000; 2000US-0065724.
10-OCT-2000; 2000US-0065729.
12-JAN-2001; 2001US-00759143.
09-FEB-2001; 2001US-00852911.
29-JUN-2001; 2001US-00852914.
10-DEC-2001; 2001US-00852914.
                                                                                                                                                                                                                                                                                                                                                                                   Xu J, Dillo
Kalos MD, F
Carter D, L
Mcneill PD,
Meagher MJ,
        The invention relates to human prostate-specific polypeptides and the polymuclectides encoding them. The invention also relates to an isolated antibody or its antigen-binding fragment that specifically binds a polypeptide of the invention, a method of detecting cancer in a patient comprising contacting a biological sample of the patient with an agent that binds a prostate-specific polypeptide and comparing the amount of bound polypeptide compared to a predetermined cut-off value and a fusion protein comprising a prostate-specific polypeptide. The sequences of the invention are used to diagnose and treat cancer, particularly prostate cancer. This sequence represents CDNA encoding a human prostate-specific polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; prostate-specific cytostatic.
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DB; ADG26745.
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Li SX, Wan
PD, Houghton
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hton RL,
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Retter MW, Stolk JA, Day Ch, Vedvick TS;
ng A, Skeiky YAM, Hepler WT, Hural J;
RL, Vinals Y De BassolsC, Foy TM, Watanabo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide;
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                                                                                                                                               CAATGGTTTCCATCACTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG
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                                   TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG
                                                                                                           CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA
                                                                                                                     CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA
                                                                                                                                                                                    AGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGGAGAATGGAGATTT
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TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA
           TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA
                                                                                 TIGITTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG
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Pred. No. 4
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RESULT 12
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ADN39812
AC ADN39
XX ADN39
XX Cance
XX Cance
XX Human
XW Fibro
XW fifta
XW vulne
XX Wound
XX Vulne
XX 13-NC
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13-FEB-2002,
20-FEB-2002;
29-MAR-2002;
04-APR-2002;
11-APR-2002;
05-UUN-2002;
16-UUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-2001;
21-NOV-2001;
29-NOV-2001;
03-DEC-2001;
04-DEC-2001;
08-JAN-2002;
10-JAN-2002;
                    Claim 8; SEQ
                                                   Determining the presence or absence of a pathological cell in a useful for diagnosing, prognosing or treating cancer, comprises a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection; diagnosis; prognosis; drug screening; dru wound healing; contraception; cytostatic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cancer/angiogenesis/fibrosis-related nucleic acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fibrotic disorder; psoriasis;
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Murray
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2001US-0334393P.
2001US-0334393P.
2001US-0335394P.
2001US-034731P.
2002US-034721P.
2002US-0347349P.
2002US-0356714P.
2002US-0356714P.
2002US-0359077P.
2002US-0368809P.
2002US-0370110P.
2002US-0370110P.
2002US-0370140P.
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                                                                                                                                                                           Ginsburg WM,
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Wilson
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E, Zlotnik
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nt; immunomodulatory;
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detecting
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whose expression is upregulated or downregulated in specific cancers or cother diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a content by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The nucleic acid of the invention, antibodies which specifically bind a culleic acid of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistation syndromes, scarring and uterine fibroids. They may calso be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 1195;
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Best Local
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14-APR-2002; 1
15-JUN-2002; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to nucleic acids and proteins (ADN38683-ADN40064) CC whose expression is upregulated or downregulated in specific cancers or cother diseases such as anglogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a cc patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The cc invention also relates to expression vectors and host cells comprising a cc nucleic acid of the invention; antibodies which specifically bind a cc polypeptide of the invention; antibodies which specifically bind a cc polypeptide of the invention; use of such antibodies for drug targeting; cc and methods of screening for modulators of activity or expression of the polypeptides and mucleic acids. The nucleic acids polypeptides, can aribodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, catherosclerosis, inflammatory diseases, autoimmune diseases, retinal convascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present expressents a nucleic acid sequence of the invention.
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Best Local Similarity
Matches 1195; Conserv
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22-JUL-2002;
09-SEP-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1195 BP; 382 A; 221 C; 233 G; 359
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Murray R,
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CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG
                                                                       CAACTTCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAACAAGTCTTGC
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R, Watson
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Pred. No. 4.4e-276;
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E, Zlotnik
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          31-MAR-2003; 2003EP-00252027
                                                                                                              Diagnostic marker; portfolio; diagnostic
                             01-OCT-2003
                                                                                                                                  Prostate cancer marker gene
                                                                                                      relative expression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           portfolio; human;
                                                                                            marker; portfolio; diagnostic parameter; gene expression;
xpression; heuristic rule; molecular diagnostic; diagnosis
cancer; breast; prostate; ovarian; colorectal; lung;
                                                                                                                                                     (first
                                                                                                                                                                                           CDNA; 1195
                                                                                                                                  STEAP,
                                                                                   gene;
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The invention relates to a method of selecting a portfolio of markers (C (e.g., genes) for use in a diagnostic parameters; (b) establishing a relationship among the diagnostic parameters; (b) establishing a relationship among the diagnostic parameters so that they are optimised; and (c) selecting CC the diagnostic parameters so that they are optimised; and (c) selecting CC application. The diagnostic parameters can include a measure of the relationship the measurement of the degree of gene, a measure of the variation in CC the measurement of the degree of gene expression, and the relationship between the diagnostic and discriminating parameters can be a mean CC variance relationship. The method further comprises the application of a comprise the application of a performing the method of the invention, and a diagnostic portfolio comprising genes selected according to the method. The method of the invention, and a diagnostic portfolio comprising gene expression. The method of the invention can be used in conjunction with any method for determining the colorectal or lung cancer). By grouping these markers into portfolios, the expression of relevant cells as well as protein-based methods of the expression of multiple genes (e.g., breast, prostate, ovarian, colorectal or lung cancer). By grouping these markers into portfolios, the most reliable results can be obtained with the smallest number of comportant in multiple-step assays such as nucleic amplification methods. The present sequence represents a human diagnostic marker gene that is a comportant in multiple assays such as nucleic amplification methods. The present sequence represents a human diagnostic marker gene that is a comportant in maltiple-step assays such as nucleic marker gene that is a comportant in maltiple and prognosing diseases for screening for prostate, or prostate, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Selecting a portfolio of markers useful in diagnostic applications comprises defining diagnostic parameters and establishing a relationship among the diagnostic parameters that identifies an optimized portfolio of markers.
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Query Match
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hes 1195;
           Similarity
100.0%; Score 1195; DB 11; ilarity 100.0%; Pred. No. 4.4e-276; Conservative 0; Mismatches 0;
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                                            C; 233 G;
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                                                      tumour-associated antigenic target; TAT; cell
                                             cytostatic;
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23-SEP-2002;
15-OCT-2002;
15-NOV-2002;
02-JUL-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the isolation of human tumour-associated antigenic target (TAT) polymucleotide and polypeptide sequences. Also disclosed is an antibody that binds to a TAT polypeptide. The antibody is a monoclonal antibody, an antibody fragment, a chimeric antibody or a humanised antibody. It is conjugated to a growth inhibitory agent. It is produced in bacteria or in CHO cells and induces death of a cell to which it binds. The antibody is useful for preparing a composition for diagnosing or treating tumours and cancer. The present sequence represents a human TAT cDNA sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibody that binds to a tumor-associated antigenic target polypeptide, useful for preparing a composition for diagnosing treating cancer.
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P-PSDB; ADL06542.
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Sequence	Compounds	Homo sapi	Mus muscu	Modulator	Sequence	Mus muscu	Mus muscu	Sequence	Sequence	Sequence	Sequence	Novel ser	Sus scrof	Sequence	Ното варі	Sequence	Sequence									

ALIGNMENTS

REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 CQ776742 LOCUS DEFINITION 문 δ B 5 밁 δ ORIGIN FEATURES source Query Match
Best Local Similarity
Matches 1195; Conserva JOURNAL 121 121 61 61 _ _ pulmonary disease pulmonary disease Patent: EP 1394274-A 428 03-MAR-2004; Genox Research, Inc. (JP) Location/Qualifiers Sequence 428 from Patent CQ776742 CQ776742.1 GI:45380132 Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H Methods of testing for bronchial asthma Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens CQ776742 Hominidae; Homo. Homo sapiens (human) GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACACCAGCATGCTAA 180 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA Conservative /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" 100.0%; Score 1195; DB 6; 100.0%; Pred. No. 5.5e-238; tive 0; Mismatches 0; Chordata; Craniata; Vertebrata; Euteleo Euarchontoglires; Primates; Catarrhini; 0; 1195 bp : EP1394274 Kubo, H., DNA ဝူ Nagai,H. and Izuhara,K. r chronic obstructive Indels Length 1195; linear PAT Euteleostomi; 0 11-MAR-2004 Gaps 60 0

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Afar,D.E., Hubert,R.S.,
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Xalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

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Xalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Vedvick,T.S., Li,S., Li,S.,
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y. Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y. Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H. Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y
Xu,J., Di, Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H
Kalos,M.D., Fanger,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
                                                                                                                                                                                                                                                                                                                                  Unclassified
                                                                                                                                                                                                                          Corixa Corporation; Seattle,
                                                                                                                                                                                                                                      Patent: US 6800746-A 878 05-OCT-2004;
                                                                                                                                                                                                                                                               Compositions and methods for the therapy
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0 1	721 ATGTGTCTCTGGGAATTGTGGGAATAGCGAATACTGGCTCTGTTGGCTGTGACATCTATTC 780	0 <
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Unknown.

Unclassified.

CE 1 (bases 1 to 1195)

RS Afar,D.E., Hubert,R.S., Leong,K., ...

Mitchell,S.C.

Mitchell,S.C.

E Peptides derived from STEAP1

JRNAL Patent: US 6887975-A 1 03-MAY-2005;

Agensys, Inc.; Santa Monica, CA
Location/Qualifiers

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ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC
                             AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT
                                                                    GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
                                                                                                   CTATTATAGCATCTCTGACTTTTCTTTACACTCTTTCTGAGGGAAGTAATTCACCCTTTTAG
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121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180	61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120 	1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60	Query Match 100.0%; Score 1195; DB 6; Length 1195; Best Local Similarity 100.0%; Pred. No. 5.5e-238; Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/or /mc /db	L Patent: WO 0151633-A 735 19-JUL-2001; CORIXA CORPORATION (US) Location/Qualifiers 1 1195		Mammalia, Eutheria, Euarchontoglires, Primates, Ca Hominidae, Homo.	Homo sapiens (human) SM Homo sapiens	AX201105 1195 bp DNA linear PAT 29-AUG-2001 ON Sequence 735 from Patent WO0151633. N AX201105 AX201105.1 GI:15390890		1141 TCAAGTTTGTATTTGTTAAAATGATTATTCAAGGAAAAAAAA	1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTTGATATATTTTATCACCAACATT 1140	1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080	961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020 	901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	841 TIGITITCCCTICTACIGGGCACAATACACGCATTGATITTTTGCCTGGAATAAGIGGATAG 900	781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840 	
RESULT 8 AX267904	P 45	, B &	y da Q	Db Qy	å å	g dy	g 99	dg Qy	p & &	Db Qy	B &	B &	S & &	DЬ	B &	S & &	§ §	Q D
904	1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAA	TGIAGAAITACTGITTACACACAIII IUG CAATAITGATATTTTATCACCA	1 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCCAGT 	961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020 	901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900	781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840	721 ATGTGTCTCTGGGATTGTGGGATTGGCATTACTGGCTCTGTTGGCTGTGGCATTCTATTC 780	1 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGGAGAATTGAGATTTT	601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660	541 TANCANGANGCAGITIGGGCTTCTCAGITICTTTTTTTGCTGTACTGCATGCAATTTATA 600 541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTGCTGTACTGCATGCA	1 ICCAMCIICAI MAIGUMACCANGIAI ANGAMGIICCACAI 1001 IOSGA ANGISCAIG 1	21	61 CAACTICCCATCAACAATATTITTATAAAATTCCCAATCCTGGTCATCAACAAAGTCTTGC 61 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAACATCTTGC 61 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAACATCTTGC	O1 CIAILA MANAGEMENTA CANCELLIA MANAGEMENTA MANAGEMENT	CTRATTRATAGAGTCTCTGACCTTTTTCTTTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG		121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180 181 AAAGACCTGTGCCTTTTGCATTTGCACCCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

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Compositions and methods for the therapy and diagnosis of prostate cancer.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Panel of nucleic acid sequences for cancer Patent: EP 1355150-A 35 22-OCT-2003; Patentical Diagnostics, Inc. (US)

Location/Qualifiers
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Mammalia; Eutheria;
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  AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA
              AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA
                                                 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTATAG
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                      TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA
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Markers for breast cancer prognosis
Patent: EP 1367138-A 35 03-DEC-2003;
Ortho Clinical Diagnostics Inc. (US)
Location/Qualifiers
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GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
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Oy 61 AATTAATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120	QY 1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60	Query Match 100.0%; Score 1195; DB 6; Length 1195; Best Local Similarity 100.0%; Pred. No. 5.5e-238; Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		JOURNAL Patent: EP 1349104-A 35 01-OCT-2003; Ortho-Clinical Diagnostics, Inc. (US) FEATURES Location/Qualifiers 1 1195	REFERENCE 1 AUTHORS Jatkoe, T. TITLE Method of selecting a portfolio of markers for use in a diagnostic application	NISM Homo sapiens Eukaryota; Me Mammalia; Eut Hominidae: Ho	1 GI:40880240	RESULT 11 AX960014 LOCUS AX960014 DEFINITION Semience 35 from Patent EP1149104	Db 1141 TCAAGTTTGTTAATAAAATGATTATTCAAGGAAAAAAAAA	1010 TOTAGAATTTACTTTATAAAAAATTTATTTATTTATTTATTT	1021	961 ITGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTCAGGAAGAAGATACTGATGAAGAAGAAGATACTGATGAAGAAGAAGATACTGATTCCTGCCATGCTTCAGGAAGAAGAAGATACTGAAGAAGAATACTGAAGAAGAAGATACTGAAGAAGAAGAAGATACTGAAGAAGAAGAAGAAGATACTGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	801 ATATAAAACAATTTGTATAGGGCACAATTACACCGCATTGATTTTGATAGAGAATAAGTGGATAG	791 CASCISIONALIGAC ELLIGACA DE CASCIANA EL CASCIANA DE CASCIANA D	721 ATGTGTCTCTGGGAATTGTGGGAATACTGGCTCTGTTGGCTGTGACATCTATTC 721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 721 ATGTGTCTCTGGGAATTGTGGGAATACTGGCTGTTTGGCTGTGACATCTATTC	661 AGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 72
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1141 TCAAGTTTGTTATTATATATATATTTTTTTTTTATGAAAAAA		AGATTAGACATGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT		901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	841 TIGITICCCTICIACIGGCACAATACACGCATIGATITITGCCIGGAATAAGIGGATAG 900 	781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840 	721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780	661 AGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGTAGTTT 720 	601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660 	541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCA	481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGG	421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480	361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420	301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360	241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300	181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240	121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

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Numbert, R.S., Vivanco, I., Chen, E., Rastegar, S., Leong, K., Mitchell, S.C., Madraswala, R., Zhou, Y., Kuo, J., Raitano, A.B., Jakobovits, A., Saffran, D.C. and Afar, D.E.

STEAP: a prostate specific cell-surface antigen highly expressed human prostate tumors

Proc. Natl. Acad. Sci. U.S.A. 96 (25), 14523-14528 (1999)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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AAAGACCTGTGCTTTTGCACTTTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT
                                                                                              GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
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                                                                    GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA
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YVSLGIVGLAILALLAVTSIPSYSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWNK
WIDDIKQFVWYTPPTFMIAVFLPIVVLIFKSILFLPCLRKKILKIRHGWEDVTKINKTE
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/product="six transmembrane epithelial antigen
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Raitano, A.B.,
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RESULT 13 CQ981397 LOCUS DEFINITION ACCESSION VERSION	0y 1 Db 1	Qy 1 Db 1	Qy 1 Db 1	Db Qy	DB Qy	B 64	B Q	Db Qy	Qy Db	₽ Q	₽ &	₽ <i>Q</i>	₽ Q	D Qy	Db Qy	Qy s	Db 1
CQ981397 1330 bp DNA linear PAT 25-JAN-2005 V Sequence 252 from Patent EP1498424. CQ981397 CQ981397.1 GI:58190687	.141 TCAAGTTTGTATTGTTAATAAATGATTATTCAAGGAAAAAAAA	081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTATCACCAACAT 	TTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 108	TACTGA 102	A 96	841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900	p — p	721 ATGTGTCTCTGGGAATTGTGGGAATACTGGCTCTGTTGGCTGTCACATCTATTC 780	ATTT 7	601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660 	541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCATGCA	81 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTT	421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480	361 CAACTTCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420 	301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360	241 CAGAACTTCAGCACACAGAGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300 	81 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 24

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Mammalia; Eutheria; E
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                                                                                                                                                                                                                CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG
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 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGACATCTATTC
                                     AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT
                                                                                    GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Pred. No. 5.4e-238;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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Compositions and
diseases
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                                          GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
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/mol_type="unassigned DN/
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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

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US-11-145-703-1
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Sequence 5979, A
Sequence 25365, A
Sequence 39315, A
Sequence 30144, A
Sequence 1, Appli
Sequence 57750, A
Sequence 51935, A
Sequence 51935, A
Sequence 46765, A
Sequence 51935, A
Sequence 2737, A
Sequence 2737, A
Sequence 45671, A
Sequence 45671, A
Sequence 152, Appl
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Sequence 25062, A
Sequence 49060, A
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367, App 40313, A	63164, A		47, Appl	~	52014, A	5, Appli	5, Appli	30480, A	51951, A	40261, A	61634, A	547, App	49, Appl	42494, A	44612, A	46490, A	5, Appli	41075, A

ALIGNMENTS

WESULT 1 US-10-750-185-59979/c US-10-750-185-59979/c Sequence 59979, Application US/10750185 Publication No. US20050260603A1 GENERAL INFORMATION: APPLICANT: MMI GENOMICS, INC. APPLICANT: MMI GENOMICS, INC. APPLICANT: MMI GENOMICS, Sue K. APPLICANT: ROSENFELD, David APPLICANT: ROSENFELD, David APPLICANT: BATES, Stephen APPLICANT: BATES, Stephen APPLICANT: PARTIN, Dennis TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS FILE REFERENCE: MMI1100-2 CURRENT APPLICATION NUMBER: US/10/750,185 CURRENT FILING DATE: 2003-12-31 PRIOR APPLICATION NUMBER: US 60/437,482 PRIOR APPLICATION NUMBER: US 60/4

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RESULT 2
US-10-750-185-25365
; Sequence 25365, Application US/10750185
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                                                                                                                                                                                                                                        76; Conservative
                                                                                                                                                                                                                                                 n 3.3%; Score 40; DB 6; Length 1687; Similarity 55.9%; Pred. No. 1.3;
                                                                                                АЛАААААААААААА 1195
                                                                                                                            TTTCATTGTTTGACATTTGTTTATTTGTTGTTTTTTAATATTTTATACTGAAGAGA
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                                                                        AGGAAAGAGAAAAGAA
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FILE REFERENCE: MMILION-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: Patentin version 3.1

SEQ ID NO 39315

LENGTH: 2464
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; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PATENTIN VERSION 3.1
; SEQ ID NO 25365
; LENGTH: 1779
; TYPE: DNA
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                                                                                                                                                        ) ORGANISM: Bovine US-10-750-185-39315
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APPLICANT: PMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-750-185-39315/c
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US-10-750-185-25365
                                                                              Matches
                                                                                              Query Match
Best Local
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Publication No. US20050260603A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.1%;
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                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MMI GENOMICS, INC. APPLICANT: DENISE, Sue K. APPLICANT: KERR, Richard
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING
                                                                                                                                                                                              TYPE: DNA
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96; Conserv
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   AGAGAAAGGGAAAATTCTGGAATATAAAATGCCATTCTGCAGTATATCTGCAGTCTCAAT 1689
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HOLM, Tom
BATES, Stephen
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Pred. No. 2.7;
0; Mismatches 9
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                                                                                                                 Length 2464;
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APPLICANT: MMI GENOMICS, INC.

APPLICANT: DANISE, Sue K.

APPLICANT: ERRR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: FANTIN, Dennis

ITILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMI1100-2

FULL REFERENCE: MMI11100-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT APPLICATION NUMBER: 003-12-31

PRIOR APPLICATION NUMBER: 060/437,482

PRIOR FILING DATE: 2002-12-31

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: Patentin version 3.1

SEQ ID NO 26044

LENGTH: 2133
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US-10-750-185-26044
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RESULT 5
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Best Local Similarity
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                                                                                                     1155 GTTAATAAAATGA 1167
                                                             1002 GTAATTACTTTGA
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                                                                                                                                                 942
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                                                                                                                                                                                                                                   882 ATAACATAATCCAGAAGTGTATATAAAACAGAAATTTCCTCATAATTCAAGAAATAACTG
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Pred. No. 3.2;
0; Mismatches 134; Indels
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US-11-145-703-1/c
; Sequence 1, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Chumakov, Ilya
; APPLICANT: Chumakov, Ilya

FILE REFERENCE: 53.US16.DIV

Bougueleret, Lydie Bihain, Bernard

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SOFTWARE: Patent.pm
SEQ ID NO 1
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PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: US 60/131,971
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/132,065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/10/147,603
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 09/539,333
PRIOR FILING DATE: 2000-03-30
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PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/146,452
PRIOR FILING DATE: 1999-07-29
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CURRENT FILING DATE: 2000-03-30
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NAME/KEY: misc_feature
LOCATION: 31..1107
OTHER INFORMATION: 5'regulatory region g35018 gene
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TYPE: DNA
ORGANISM: Homo sapiens
                                               NAME/KEY: exon
LOCATION: 65505..65853
OTHER INFORMATION: exon
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LOCATION: 29967..30282
OTHER INFORMATION: exor
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LOCATION: 29388..29502
OTHER INFORMATION: exon
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LOCATION: 1108..1289
OTHER INFORMATION: ex
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OTHER INFORMATION: exon
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OTHER INFORMATION:
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LOCATION: 14877..14920
OTHER INFORMATION: exor
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OTHER INFORMATION: exo
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AME/KEY: misc_feature
OCATION: 65854..67854
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PPLICANT: Essioux, Laurent TILE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKE &
                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 231787..231880
OTHER INFORMATION: exon (
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LOCATION: 230408..230721
OTHER INFORMATION: exon
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LOCATION: 215819..215975
LOCATION: exon
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NAME/KEY: exon
NAME/KEY: 215819..215941
NAME/KEY: exon R
FEATURE:
NAME/KEY: exon
LOCATION: 237406..237428
OTHER INFORMATION: exon Nbis complement g34872 gene
                                                                                                                                                         OTHER INFORMATION:
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LOCATION: 231870..231879
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LOCATION: 231272..231412
OTHER INFORMATION: exon Obis
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LOCATION: 229647..229742
LOCATION: AMERICAN EXON X
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LOCATION: 216661..217061
OTHER INFORMATION: exon Q complement g34872 gene
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LOCATION: 213818..215818
OTHER INFORMATION: 3'regulatory region g34872 gene
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LOCATION: 216836..216915
OTHER INFORMATION: exon '
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LOCATION: 94124..94964
                                                                                OTHER INFORMATION:
                                                                                                NAME/KEY: exon
LOCATION: 234174..234321
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LOCATION: 216661..216952
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OTHER INFORMATION:
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OTHER INFORMATION:
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OCATION: 215702..215746
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OCATION: 217027..217061
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)RMATION: exon T g35030 gene
                                                                              exon O complement g34872 gene
                                                                                                                                                       exon O1
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Best Local
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LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory region g34872 gene
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LOCATION: 240528...240994
OTHER_INFORMATION: exon M692 complement
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LOCATION: 240528..240596
OTHER INFORMATION: exon M1090
                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: 3'regulatory region g34665 gene
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LOCATION: 290652..292652
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LOCATION: 240800..240993
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LOCATION: 240528..241685
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LOCATION: 240528..240824
OTHER INFORMATION: exon M862
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OTHER INFORMATION: exon MS2
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LOCATION: 240528..240569
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LOCATION: 239719..239853
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LOCATION: 239719..239807
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LOCATION: 240528..240617
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                                                                                      GAATTACTGTTTACACACACATTTTTTGTTCAATATTGATATATTTTATCACCAACATTTCAA 1144
                                                                                                                                                                                                                                                                        AAACCAACTGTTATGTTTTCTTTTCAGTGAGTTTATGGTAGTCTTTTAAAAATCACATTGG
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                                                                                                                                                                                                     TAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTGTA 1084
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Pred. No. 29
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US-10-750-185-36894/c
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LENGTH: 1443
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SEQ ID NO 36894
LENGTH: 1301
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                                                                           Matches 104;
                                                                                           Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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APPLICANT: DeNISS, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENPELD, David
                                                                                                                                                                                                                                                      FILE REFERENCE: MMII100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MMI GENOMICS, INC. APPLICANT: DENISE, Sue K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Bovine
                                                                                                                                                                             ORGANISM: Bovine
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                                  980 AAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGA 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        851 TGCAGACATTTTAATTCTCCAAAATTGTGTTTTGTGTTTTAATTCTCCAAGATTGTGTTCT 792
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                                                                         3.1%;
ilarity 48.4%;
Conservative
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                                                                                             Score 37.4; D. Pred. No. 5.3;
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                                                                             Mismatches
                                                                                                                  DB 6;
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GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC.

APPLICANT: MERISE, Sue K.

APPLICANT: KERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: HOLM, Tom

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOY

FILE REFERENCES: MMILIO-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31
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Best Local Similarity
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US-10-750-185-51935
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US-10-750-185-32077/c
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SEQ ID NO 32077
LENGTH: 1495
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1046 CACCAAAATTAACAAAACTGAGATATGTTCCCAGTTGTAGAATTACTGTTTACACACATT 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1160 TAAAATGATTATTCAAGGAAAAAAAAAAAAAAAA 1194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATTATTCAAGGAAAAAAAAAAAAAAAA 1194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTGTTCAATATTGATATTTTTATCACCAACATTTCAAGTTTGTATTTGTTAATAAAAT 1165
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Pred. No. 6.8;
0; Mismatches
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                                                                          BOVINE
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; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-46765
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US-10-750-185-51383/c
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  Sequence 51383, Application US/10750185
Publication No. US20050260803A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
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; SOFTWARE: PatentIN version 3.1

; SEQ ID NO 51935

; LENGTH; 1798

; TYPE: DNA

; ORGANISM: Bovine 19866880871.

US-10-750-185-51935
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                                                                                                                                                                                                                                                                                                 Query Match 3.1%; Score 36.8; Dest Local Similarity 52.6%; Pred. No. 8.2; Matches 80; Conservative 0; Mismatches
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Best Local Similarity 62.4%;
Matches 58; Conservative
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APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
                                                                                                                                                  1104 TTTTTGTTCAATATTGATATTTTATCACCAACATTTCAAGTTTGTATTTGTTAATAAA 1163
                                                                                                                                                                                                                                                1044 GTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTGTAGAATTACTGTTTACACACA 1103
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AATATATTACTGGGAAAAGGTTAAAAAATAAA 1473
                                            АТGATTATTCAAGGAAAAAAAAAAAAAAA 1195
                                                                                                GTCTTTATTAAAATATGAATGTTGTTGTTGTAGTTACTATGCAACTCTTGACACTGC 1381
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                                                                                                                                                                                                                                                                                                                                                DB 6;
                                                                                                                                                                                                                                                                                               72;
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: WMII100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER: OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 51383
LENGTH: 2081
TYPE: DNA
ORGANISM: Bovine 19866880958299
US-10-750-185-51383
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RESULT 13
US-11-099-691-22
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; SEQ ID NO 52737
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Bovine 19866881330166
US-10-750-185-52737
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US-10-750-185-52737/c
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APPLICANT:
APPLICANT:
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
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NUMBER OF SEQ ID NOS: 64922
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Local Similarity 57.4%;
nes 66; Conservative
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                                                                                                              1080 TTGTAGAATTACTGTTTACACACATTTTTTGTTCAATATTTGATATATTTTTATCACCAACAT 1139
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                                                                           TTATAGCAAAATTATTTTCCAGTATTTTTTTAAAAAACTAGAGCTATTTTATAGGGGATAC 286
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KERR, Richard
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58.0%;
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Pred. No. 8.7;
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMIL100-2
FILE REFERENCE: MMIL100-2
FILE REFERENCE: MMIL100-2
FILE REFERENCE: MMIL100-3
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APPLICANT: BAUGHM, Mariah R.
APPLICANT: YANG, Jumming
TITLE OF INVENTION: CELL SIGNALING PROTEINS
FILE REFERENCE: PF-0521 PCT
CURRENT APPLICATION NUMBER: US/11/099,691
CURRENT FILING DATE: 2005-04-06
PRIOR APPLICATION NUMBER: US/09/700,444
PRIOR APPLICATION NUMBER: US/09/700,444
PRIOR APPLICATION NUMBER: 05/085,343
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,010
PRIOR APPLICATION NUMBER: 60/098,010
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SEQ ID NO 22
LENGTH: 2948
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MMI GENOMICS, INC. APPLICANT: DENISE, Sue K. APPLICANT: KERR, Richard
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les 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1094 TTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCAAGTTTGTATT 1153
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YUE, Henry
TANG, Y. Tom
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Pred. No. 1
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Length 1577;
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Query Match

3.0%;

Score 36.2;

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GENERAL INFORMATION.

GENERAL INFORMATION.

APPLICANT: MMI GENOMICS, INC.

APPLICANT: MERCH, Richard

APPLICANT: KERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: BATES, Stephen

APPLICANT: FANTIN, Dennis

FILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMILLOO-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

FRIOR APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31

FRIOR FILING DATE: 2002-12-31

FRIOR FILING DATE: 2002-12-31

SOPTWARE: PASCENTIAN VERSION 3.1

SEQ ID NO 42808

TYPE: DNA

TYPE: DNA
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; ORGANISM: Bovine 19866880681507
US-10-750-185-42808
Search completed: December 5, 2005, 08:05:49 Job time: 379.544 secs
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US-10-750-185-42808/c
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                                                                                           1509
                                                                                                              1079 GTTGTAGAATTTACTGTTTACACACACATTTTTTGTTCAATATTTGA--TATATTTTTATCACCAA 1136
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Sequence 215, App	Sequence 215, App	•	•	•	Sequence 215, App	Sequence 215, App	Sequence 215, App	Sequence 215, App	Sequence 215, App	Sequence 215, App	Sequence 6, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 7, Appli	Sequence 10, Appl	Sequence 5, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 993, App	Sequence 995, App

ALIGNMENTS

US-09-323-873A-1 US-09-323-873A-1 PRIOR APPLICATION NUMBER: 60/087,520 PRIOR FILING DATE: 1998-06-01 PRIOR APPLICATION NUMBER: 60/091,183 PRIOR FILING DATE: 1998-06-30 NUMBER OF SEO ID NOS: 32 SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1 GENERAL INFORMATION: Sequence 1, Application US/09323873A Patent No. 6329503 Query Match 100.0%; Score 1195; DB 3; Best Local Similarity 100.0%; Pred. No. 6.6e-301; Matches 1195; Conservative 0; Mismatches 0; APPLICANT: Daniel E. Afar APPLICANT: Rene S. Hubert APPLICANT: Kahan Leong APPLICANT: Kahan Leong APPLICANT: Douglas C. Saffran APPLICANT: Douglas C. Saffran APPLICANT: Steve Chappell Micchell TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THE FILE REFERENCE: 129.16USUZ CURRENT APPLICATION NUMBER: US/09/323,873A CURRENT FILING DATE: 1999-06-01 LENGTH: 1195 TYPE: DNA ORGANISM: Homo Sapiens 4.0 AND USES THEREOF Length 1195;

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AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACACCAGCATGCTAA 180

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61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA

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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Fenger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Use, Craig H.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: DIAGNOSIS OF PROSTATE CAL
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CAL
TITLE REFERENCE: 210121.427021
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEO ID NOS: 898
SOFTWARE: FBSTSEQ for Windows Version 3.0
SEO ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
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   GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC
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Pred. No. 6.6e-301;
; Mismatches 0;
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US-09-679-426-878

Sequence 878, Application US/09679426

Patent No. 6759515

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Kalos, Michael D.

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Li, Samuel

APPLICANT: Li, Samuel

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Mang, Aijun

APPLICANT: Hepler, William

APPLICANT: Hepler, William

APPLICANT: Negley, Yasir A.W.

APPLICANT: Negley, Yasir A.W.

APPLICANT: David Compositions and METHOD

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE C

FILE REFERENCE: 210121.427C20

CURRENT FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 895

SOPTMARE: PastSEQ for Windows Version 3.0

SEQ ID NO 878

LENGTH: 1195
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TYPE: DNA
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APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-759-143-878
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Patent NO. 6800746
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jenni
APPLICANT: Mitcham, Jenni
APPLICANT: Harlocker, Sus
APPLICANT: Harlocker, Sus
APPLICANT: Henderson, Rob
APPLICANT: Henderson, Rob
APPLICANT: Kalos, Mitchael
APPLICANT: Retter, Marc W
APPLICANT: Rotter, Marc W
APPLICANT: Stolk, John A
APPLICANT: Day, Craig H
APPLICANT: Day, Craig H
APPLICANT: Carter, Darric
APPLICANT: Carter, Darric
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APPLICANT: Carter, Darric
APPLICANT: Skeiky, Yasir
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US-09-759-143-878
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Best Local Similarity
Matches 1195; Conserv
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Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                         AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT
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Sequence 1, Application US/10010667A
Patent No. 6887975
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene S.
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: NOVEL SERPENTINE TH
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US-10-010-667A-1
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FILE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND FILE REFERENCE: 511502001601
CURRENT APPLICATION NUMBER: US/10/010,667A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1195
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                                                             AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT
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APPLICANT: Fanger, Gary R.

APPLICANT: Wantanabe, Yoshihiro

APPLICANT: Wantanabe, Yoshihiro

APPLICANT: Wadgher, Maddleine Joy

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 21011.427C27

CURRENT APPLICATION NUMBER: US/10/012,896

CURRENT FILING DATE: 2001-12-10

NUMBER OF SEQ ID NOS: 1011

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 878

LENGTH: 1195

TYPE: DNA

ORGANISM: Homo sapiens
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
US-10-012-896-878
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Patent No. 694323
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Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Vedvick, Thomas S.
Carter, Darrick
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APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.17-US-I1
CURRENT APPLICATION NUMBER: US/09/455,486
CURRENT FILING DATE: 1999-12-06
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1193
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (64)...(1083)
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Best Local Similarity
Matches 1193; Conserva
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ATGGTTTCCATCACCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTC
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRANCESEQ for Windows Version 4.0
SEQ ID NO 2686
LENGTH: 1147
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US-09-949-016-2686
                                                                                                                                                                                                                                                              Sequence 2686, Application US/09949016 Patent No. 6812339
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US-09-949-016-2686
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Pred. No. 1.7e-287;
0; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6329503
GENERAL INFORMATION:
APPLICANT: Beniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 6
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Best Local Similarity
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APPLICANT: Douglas C. Saifran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo Sapiens
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CAACTTCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC
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Pred. No. 1.2e-204;
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SEQ ID NO 4
LENGTH: 3627
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity 99.5%;
                                                                                                                                                                                                                Matches 828;
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APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: MOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THER
FILE REFERENCE: 129.17-US-II
CURRENT APPLICATION NUMBER: US/09/455,486
CURRENT FILING DATE: 1999-12-06
CURRENT FILING DATE: 1999-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA
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Pred. No. 1.2e-204;
0; Mismatches 4;
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US-10-010-667A-6

(Sequence 6, Application US/10010667A

Patent No. 6887975

GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION NUMBER: US/10/010,667A

CURRENT APPLICATION NUMBER: US/10/010,667A

CURRENT FILING DATE: 1998-06-01

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1998-06-01

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1998-06-30

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 3627

TYPE: DNA

GRGANISM: Homo sapiens

US-10-010-667A-6
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; Sequence 342, Application US/09439313
Patent No. 6329505
; GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.

RESULT 12 US-09-439-313-342/c

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                                              ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC
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Pred. No. 1.2e-204;
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APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT APPLICATION NUMBER: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 592
TYPE: NNA
RESULT 13
US-09-352-616A-342/c
US-09-352-616A-342/c
; Sequence 342, Application U;
; Patent No. 6395278
; Patent No. 6395278
; APPLICANT: Dillon, Davin (
; APPLICANT: Harlocker, Sus;
; APPLICANT: Jiang, Yuqui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennii
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Jiang, Yuqui
Xu, Jiangchun
Mitcham, Jennifer Lynn
                                                             MATION:
Dillon, Davin C.
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; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE; FILE REFERENCE: 210121.427C8; CURRENT APPLICATION UNMBER: US/09/352,616A; CURRENT FILLING DATE: 1999-07-13; NUMBER OF SEQ ID NOS: 472; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 342; LENGTH: 592; TYPE: DNA GRGANISM: Homo Bapien
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Pred. No. 2.6e-141;
1; Mismatches 1;
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Sequence 342, Application US/09636215
Patent NO. 6620922
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Marlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Handerson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
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US-09-636-215-342/c
  APPLICANT:
Stolk, John
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TAACAAGAAAGCARATTGGGCTTCTCAGTTTCTTTTTGCTGT

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APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: West, William
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
ITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
ITILE OF INVENTION NUMBER: US/09/636,215
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FABLSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 592
TYPE: DNA
ORGANISM: Homo Bapien
US-09-636-215-342
RESULT 15
US-09-685-166A-342/c
US-09-685-166A-342/c
Sequence 342, Application US/0968
Patent No. 6630305
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Usedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Weang, Aljun
APPLICANT: Weang, Aljun
APPLICANT: Hepler, William
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
ITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
ITILE OF INVENTION UMMBER: US/09/685, 166A
CURRENT APPLICATION NUMBER: US/09/685, 166A
CURRENT PILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 592
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; ORGANISM: Homo sapien
US-09-685-166A-342
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Matches 581; Conservative
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2: /cgn2 6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

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4: /cgn2 6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*

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7: /cgn2 6/ptodata/1/pubpna/USOP_PUBCOMB.seq:*

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	ָרָי.	r, Susan uqui	Harlocke Jiang, Y	APPLICANT:	
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Sequence 878 Application US/09780669

Patent No. US20020051977A1

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Kalos, Michael D.

APPLICANT: Stolk, John A.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Li, Samuel

APPLICANT: Hepler, William

APPLICANT: Hepler, William

APPLICANT: Houghton, Raymond L.

APPLICANT: Mcneill, Patridla D.

APPLICANT: Moughton, Raymond L.

APPLICANT: Moughton, Raymond L.

APPLICANT: Moughton, Raymond L.

APPLICANT: APPLICATION NUMBER: US/09/780,669

CURRENT APPLICATION NUMBER: US/09/780,669

CURRENT FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 943

SOFTMARE: FastESEQ for Windows Version 3.0

SEQ ID NO 878

LENGTH: 1195

TYPE: DNA

ORGANISM: Homo sapiens
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RESULT 3

US-09-822-827-878

Sequence 878, Application US/09822827

Patent No. US20020081680A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCE FILE REFERENCE: 210121.534C1

CURRENT APPLICATION NUMBER: US/09/822,827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FeastSEQ for Windows Version 3.0

SEQ ID NO 878

LENGTH: 1195

TYPE: DNA

ORGANISM: Homo sapiens

US-09-822-827-878
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1195; Conservative 0
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Score 1195; DB 3;
Pred. No. 1.1e-281;
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APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEI
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-66-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-793-878
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Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
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Best Local Similarity
Matches 1195; Conserv
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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   Sequence 878, Application US/098958

Publication No. US20020193296A1

GENERAL INFORMATION:

APPLICANT: Nu, Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqiu

APPLICANT: Kalos, Michael D.

APPLICANT: Retter, Marc W.
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Jiang, Yuqiu
Kalos, Michael D.
Retter, Marc W.
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APPLICANT: Foy, Teresa
APPLICANT: Foy, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT FILING DATE: 2001-06-29
RUMBER OF SEQ ID NOS: 990
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-814-878
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Best Local Similarity
Matches 1195; Conserv
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
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Vedvick, Thomas
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Publication No. US200201832
GENERAL INFORWATION:
APPLICANT: Xu Jiangchun
APPLICANT: Dillon, Davin
APPLICANT: Mitcham, Jenni
APPLICANT: Harlocker, Sus
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           APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
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Vedvick, Thomas
Carter, Darrick
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
Henderson, Robert
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CURRENT FILING DATE: 2001-12-10

NUMBER OF SEQ ID NOS: 1011

SOFTWARE: FastSEQ for Windows Version 3.

SEQ ID NO 878

LENGTH: 1195

TYPE: DNA

ORGANISM: Homo sapiens
US-10-012-896-878
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Sequence 1, Application US/10011095

| Publication No. US20030045682A1 |
| GENERAL INFORMATION: AFPLICANT: AFPLICANT: Hubert, Rene S. APPLICANT: Hebert, Rene S. APPLICANT: Leong, Kahan APPLICANT: Hatchell, Steve Chappell APPLICANT: Mitchell, Steve Chappell TITLE OF INVENTION: ANTIBODIES IMMUNOSPECIFIC FOR STEAP1 (AS AMENDED) FILE REFERENCE: 511582001610 |
| CURRENT APPLICATION NUMBER: US/10/011,095 |
| CURRENT FILING DATE: 1091-12-06 |
| PRIOR APPLICATION NUMBER: 60/087,520 |
| PRIOR APPLICATION NUMBER: 60/087,520 |
| PRIOR FILING DATE: 1998-06-01 |
| PRIOR APPLICATION NUMBER: 60/091,183 |
| PRIOR FILING DATE: 1998-06-30 |
| NUMBER OF SEQ ID NOS: 32 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| LENGTH: 1195 |
| LENGTH: 1195 |
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TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO
FILE REFERENCE: 511582001601
CURRENT APPLICATION NUMBER: US/10/010,667A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOPTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1195
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; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-010-667A-1
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Pury Match 100.0%; Score 1195; DB 5; Length 1195; Best Local Similarity 100.0%; Pred. No. 1.1e-281;	LENGTH: 1195 TYPE: DNA ORGANISM: Homo sapiens	PRIOR FILING DATE: 2002-03-05 NUMBER OF SEQ ID NOS: 455 SOFTWARE: FastSEQ for Windows Version 4.0	PRIOR FILING DATE: 2001-09-25 PRIOR PELING DATE: 2001-09-25 PRIOR APPLICATION NUMBER: 60/341,746 PRIOR FILING DATE: 2001-12-12 PRIOR APPLICATION NUMBER: 60/362,158	PRIOR FILING DATE: 2001-07-25 PRIOR APPLICATION NUMBER: 60/314,356 PRIOR FILING DATE: 2001-08-22 PRIOR FILING TATE: 2001-08-22 PRIOR FILING TATE: 2001-08-22	INVENTION: 115KAFT OF ERENCE: MRI-044 APPLICATION NUMBER: US/: FILING DATE: 2002-07-2:	APPLICANT: Ander, Aumer APPLICANT: Anderson, Dustin TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: METHODS FOR DENTIFICATION, ASSESSMENT, PREVENTION, AND	Kamat Wonse	APPLICANI: Monarat, North E. APPLICANI: Endege, Wilson O. APPLICANI: Gannavarapu, Manjula APPLICANI: Gorbatcheva, Bella APPLICANI: Hospet Gobatcheva, Bella	S S S	2SULT 9 3-10-205-823-396	1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAA	1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTTGATATATTTTATCACCAACATT 1140 	1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080 	961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020 	901 ATATAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900	781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840	721 ATGTGTCTCTGGGAATTGTGGGAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
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APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ta
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DUA
ORGANISM: Homo sapiens
US-10-144-678A-878
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US-10-144-678A-878
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Publication No. US20030157089A1
GENERAL INFORMATION:
APPLICANT: Xu Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Best Local Similarity
Matches 1195; Conserv
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Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Skeiky, Yasir A. W.
Hepler, William T.
Hural, John
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Vedvick, Thomas
Carter, Darrick
Li, Samuel X.
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Houghton, Raymond L.
Vinals y de Bassols,
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                                                       Sequence 878, Applic Publication No. US20 GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
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                                                                      Application US/10294025

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; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE (
FILE REFERENCE: 2.10121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEO ID NOS: 1038
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 878
; ENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
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Sequence 35, Application US/10393590

Publication No. US/2030190656A1

GENERAL INFORMATION:

APPLICANT: WANG, YIXIN

TITLE OF INVENTION: BREAST CANCER PROGNASTIC POINTERING PRICE COS 268 US NP

CURRENT APPLICATION NUMBER: US/10/393,590

CURRENT FILING DATE: 2003-03-21

PRIOR FILING DATE: 2003-03-29

PRIOR FILING DATE: 2003-03-29

NUMBER OF SEQ ID NOS: 100

CONTENTS PRIOR DATE: 2012-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 35
LENGTH: 1195
TYPE: DNA
ORGANISM: human
US-10-393-590-35
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Best Local Similarity 100.0%;
Matches 1195; Conservative (
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Sequence 35, Application US/10393567 Publication No. US20030194733A1 GENERAL INFORMATION: APPLICANT: WANG, YIXIN TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL FILE REFERENCE: CDS 269 US NP CURRENT APPLICATION NUMBER: US/10/393,567 CURRENT FILING DATE: 2003-03-21 PRIOR APPLICATION NUMBER: 60/368,667 PRIOR PILING DATE: 2002-03-29 NUMBER OF SEQ ID NOS: 100 SOFTWARE: Patentin version 3.1 SEQ ID NO 35 LENGTH: 1195 TYPE: DNA	mm m v	Db 1021 AGATTAGACATGGTTGGGAAGACGTCACAAAATTAACAAAACTGAGATATGTTCCCAGT 1080 Qy 1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTTGATATATTTTATCACCAACATT 1140	961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA	Qy 901 ATATAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	OY 841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900	QY 781 CATCTGTGAGTGACTCTTTGACATGGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840	Qy 721 ATGTGTCTCTGGGAATTGTGGGAATTGGCAATACTGGCTGTGTGACATCTATTC 780	Qy 661 AGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGGAGAATGGAGATTT 720	Oy 601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660	Oy 541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCA	Qy 481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGG	QY 421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480	Db 361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
	Qy 661 AGGTCCAACAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGAGATTT 720	Db 541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCAAGTTTATA 600 OY 601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660	481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGG	OY 421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480	QY 361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAGTCTTGC 420	Qy 301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360	Qy 241 CAGAACTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300	QY 181 AAAGACCTGTGCGTTTTGCATTTTGCACCAAACAGCCCATGCTGATGAGTTTGACTGCCCTT 240	QY 121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACCACGGGAGAGACCAGCATGCTAA 180	Qy 61 AATTAATGGAAAGCAGAAAAGAACTATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120	QY 1 CCGAGACTCACGTCAAGCTAAGGCGAAGAGTGGGTGGAAGCCATACTATTTATAG 60 [Query Match 100.0%; Score 1195; DB 6; Length 1195; Best Local Similarity 100.0%; Pred. No. 1.1e-281; Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	; ORGANISM: human US-10-393-567-35

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Sequence 35, Application US/10394087
Publication No. US20030194734A1
GENERAL INFORMATION:
APPLICANT: Jatkoe, Tim
FILE OF INVENTION: SELECTION OF MARKERS
FILE REFERENCE: CDS 265 US NP
CURRENT APPLICATION NUMBER: US/10/394,087
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: 60/368,790
PRIOR PILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35
LENGTH: 1195
TYPE: DNA
ORGANISM: human
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                                     CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG
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100.0%; Pred. No. 1.1e-281;
tive 0; Mismatches 0;
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US-10-295-027-713
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APPLICANT:
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APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 713, Applic Publication No. US20 GENERAL INFORMATION:
APPLICANT: EOS Biotechnology, Inc.
APPLICANT: EOS Biotechnology, Inc.
APPLICANT: EOS Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer File Reference: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 99/663,733
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2000-09-15
PRIOR PILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-15
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Glynne, Richard
Hevezi, Peter A.
Mack, David H.
Murray, Richard
Watson, Susan R.
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PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILLING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR PILLING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR PILLING DATE: 2001-12-14
PRIOR PILLING DATE: 2001-12-14
PRIOR PILLING DATE: 2002-01-08
PRIOR FILLING DATE: 2002-01-08
PRIOR FILLING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILLING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILLING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/356,714
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; ORGANISM: Homo sapiens
US-10-295-027-713
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Best Local Similarity
Matches 1195; Conserv
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Search completed: December 5, 2005, 07:54:08 Job time : 1120.59 secs

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-Q-/Ggn2_1/USPTO_Spool h/US1075062/runat 06122005 162947_15675/app_query.fasta_1.519
-DBs-Published_Applications_NA_Main_-OPMT=Fastap_-SUFFIX=xnpbm_-MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bIts -START=1 =END=-1 -MATRIX=bLosum62
-TRANS=human40.cdi -LIST=45 -DCCALIGN=200 -THR_SCORE=pot -THR_MX=100
-THR_MIN=0 -ALIGN=15 -MODB=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000000 -USER=US10750262_@CGN_1 1 1026_@runat_06122005_162947_15675
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT_-DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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US-10-830-899-2

US-10-752-421-1
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ALIGNMENTS

RESULT 1 US-10-696-639-15

Sequence 15, Application US/10696639 Publication No. US20050037439A1

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GENERAL INFORMATION:
APPLICANT: Boarmacia Corporation
APPLICANT: DIPERENTIALIY
APPLICATION NUMBER: US/10/696,639
CURRENT FILING DATE: 2003-10-29
NUMBER: G0/422,176
PRIOR APPLICATION NUMBER: 60/422,176
PRIOR FILING DATE: 2002-10-29
NUMBER: 60/422,176
PRIOR APPLICATION NUMBER: 60/422,176
PRIOR FILING DATE: 2002-10-29
NUMBER: 60/422,176
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NUMBER: 60/422,176
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RESULT 2
US-10-165-044-1
; Sequence 1, Application US/10165044
; Publication No. US20030149531A1
; GENERAL INFORMATION:
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APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas Saffran
APPLICANT: Douglas Saffran
APPLICANT: Steven Chappell Mitchell
APPLICANT: Steven Chappell Mitchell
APPLICANT: Mary Faris
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: $1158-20016.02
CURRENT APPLICATION NUMBER: US /10/165,044
CURRENT FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR APPLICATION NUMBER: WS 09/62941
PRIOR APPLICATIO
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Best Local Similarity:
Query Match:
DB:
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NAME/KEY: CDS
LOCATION: (64).
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              CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
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Matches:
Conservative:
Mismatches:
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APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOI
CURRENT APPLICATION UNMBER: US/10/408,009
CURRENT APPLICATION NUMBER: 09/455,486
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILLING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILLING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 1193
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY. CDS
            Alignment Scores: Pred. No.:
                                                  US-10-408-009-1
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US-10-408-009-1
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                                                          NAME/KEY: CDS
LOCATION: (64)...
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Best Local Similarity:
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ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu
                      SerLeuLeuLeuGlyThr1leHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle
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Conservative:
Mismatches:
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1083)
US-10-857-785-1
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PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 60/087,520
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 47
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APPLICANT: Daniel E.
APPLICANT: Rene S.
APPLICANT: Arthur I
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DB:
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Publication No. US20040219162Al
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SEQ ID NO 1
LENGTH: 1193
TYPE: DNA
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APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THE
FILE REFERENCE: 511582001607
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CURRENT FILING DATE: 2004-05-28
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APPLICANT: Daniel E. Afar
APPLICANT: Archur B. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
APPLICANTON NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION. EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 511582001606
CURRENT APPLICATION NUMBER: US/10/856,109
CURRENT APPLICATION NUMBER: US 09/455,486
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR APPLICATION NUMBER: US 60/087,520
PRIOR APPLICATION NUMBER: US 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: US 60/097,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FABSEEQ for Windows Version 4.0
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                                                LENGTH: 11
TYPE: DNA
                  ORGANISM: Homo sapiens FEATURE:
NAME/KEY: CDS
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US-10-856-109-1
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TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC
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APPLICAVI: Gudas, Jean
APPLICAVI: APPLICAVI: Altano, Arthur B.
TITLE OF INVENTION: Antibodies and Molecules Derived
TITLE OF INVENTION: therefrom that Bind to STEAP-1 Pro
FILE REFERENCE: 51158-20016.26
CURRENT FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: 09/123,873
PRIOR APPLICATION NUMBER: 09/123,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 10/010,667
PRIOR APPLICATION NUMBER: 10/010,95
PRIOR APPLICATION NUMBER: 10/011,095
PRIOR APPLICATION NUMBER: 10/336,878
PRIOR APPLICATION NUMBER: 10/336,878
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR APPLICATION NUMBER: 00/91,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 10/336,878
PRIOR APPLICATION NUMBER: 00/91,183
PRIOR APPLICATION NUMBER: 00/91,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 103
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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APPLICANT: Jakobovits, Aya
APPLICANT: Etessami, Soudabeh
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Juan
APPLICANT: Meyrick Morrison, Karen Ja
APPLICANT: Meyrick Morrison, Karen Ja
APPLICANT: Jia, Xiao-Chi
APPLICANT: Faris, Mary
APPLICANT: Gudas, Jean
APPLICANT: Gudas, Jean
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US-10-830-899-2
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ORGANISM: Homo Bap
FEATURE:
FEATURE:
NAME/KEY: CDS
LOCATION: (66)...(
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                                   CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA
                                                          ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
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LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysIleAlaAlaIle
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APPLICANT: Agensys, Inc.
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas Saffran
APPLICANT: Douglas Saffran
APPLICANT: Daniel E.H. Afar
APPLICANT: Steven Chappell Mitchell
APPLICANT: Mary Faris
APPLICANT: Mary Faris
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO
FILE REFERENCE: 51158-20016-02
CURRENT APPLICATION NUMBER: US/10/753,195
CURRENT FILING DATE: 2004-01-06
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Publication No. US20050004349A1
GENERAL INFORMATION:
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PRIOR PILLING DATE: 2002-06-06
PRIOR PILLING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: US 60/087,520
PRIOR FILLING DATE: 1998-06-01
PRIOR PILLING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR FILLING DATE: 1999-06-01
PRIOR FILLING DATE: 1990-06-01
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US-10-752-421-1

US-10-752-421-1

Sequence 1, Application US/10752421

Publication No. US2005063975A1

GENERAL INFORMATION:

APPLICANT: Daniel E. Afar

APPLICANT: Noniel E. Afar

APPLICANT: Noniel E. Afar

APPLICANT: Stephen C. Mitchell

TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF

FILE REFERENCE: 511582001612

CURRENT APPLICATION NUMBER: US/10/752,421

CURRENT APPLICATION NUMBER: US/09/455,486

PRIOR APPLICATION NUMBER: US/09/323,873

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: US/99/323,873

PRIOR FILING DATE: 1999-06-01

PRIOR FILING DATE: 1999-06-01

PRIOR APPLICATION NUMBER: US/09/323,873

PRIOR FILING DATE: 1998-06-01

PRIOR FILING DATE: 1998-06-01

PRIOR FILING DATE: 1998-06-30

NUMBER OF SEQ ID NOS: 47

SOFTWARE: FRANCESCE OF Windows Version 4.0

LENGTH: 1193

TYPE: DNA
                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1083)
US-10-752-421-1
                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                  US-10-861-662-2
; Sequence 2, Application US/10861662
; Publication No. US20050086707A1
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                                                                                 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080
                                                                                                 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
                                                                                                                                                                                          ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysIleLeuLysIle 320
                                                                                                                                                                                                                                              SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpTleAspIle
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APPLICANT: Rallano, Arthur B.
APPLICANT: Rallano, Arthur B.
TITLE OF INVENTION: Antibodies and Molecules Derived
TITLE OF INVENTION: Antibodies and Molecules Prot
FILE REFERENCE: 51158-20016.26
CURRENT APPLICATION NUMBER: US/10/861,662
CURRENT FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-66-01
PRIOR FILING DATE: 10901-12-06
PRIOR APPLICATION NUMBER: 10/011,095
PRIOR APPLICATION NUMBER: 10/011,095
PRIOR FILING DATE: 2001-12-06
PRIOR PRILING DATE: 2001-12-06
PRIOR PRILING DATE: 2001-05-06
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 09/425,486
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR APPLICATION NUMBER: 09/65,486
PRIOR APPLICATION NUMBER: 00/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
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APPLICANT: Jakobovits, A
APPLICANT: Etessami, Sc
APPLICANT: Challita-Eic
APPLICANT: Perez-Villar
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DB:
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US-10-861-662-2
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Best Local Similarity:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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ORGANISM: Homo
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                                                          101 SerHisGlnGlnTyrPheTyrLysIleProIléLeuValIleAsnLysValLeuProMet 120
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Challita-Eid, Pia M.
Perez-Villar, Juan
Meyrick Morrison, Karen Jane
Jia, Xiao-Chi
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Gudas, Jean
Val Ser Ile Thr Leu Leu Ala Leu Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln
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FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 878
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                                                             APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
FILE REFERENCE: 210121.47C23
                                                                                                                                           APPLICANT:
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Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S
Carter, Darrick
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Harlocker, Susan L
Jiano
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-878
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Db 906	6 AAACAATTIGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC
Оу 301	ValLeullePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 32
Db 966	6 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025
0у 32	
Db 1026	AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG
RESULT 11 US-09-780-66 ; Sequence 8	9-878 78, Application US/09780669
GENERAL	
; APPLICANT	: Xu, Jiangchun : Dillon, Davin C.
	Mitcham, Jennifer
	Kalos, Michael D. Fanger, Gary R
	Retter, Marc W.
APPLICANT:	Day, Craig H.
; APPLICANT	Carter, Darrick
APPLICANT:	Wang Aijin
, APPLICANT	Skeiky, Yasir A.W.
; APPLICANT:	Hepier, William Hural, John
; APPLICANT:	McNeill, Patricia D.
; TITLE OF I	ND METHO
FILE REFER	NVENTION: DIAGNOSIS OF PROSTATE CANCER ENCE: 210121.427C24
; CURRENT AP	ION NUM
; SOFTWARE:	SEQ 1D NOS: 943 FastSEQ for Windows Version 3.0
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TYPE: DN ORGANISM	Homo sapiens
	878
Pred. No.:	: 1.67e-195 Length: 11
ent ent	1790.00 Matches: 339
Best Local Similar Query Match:	rity: 100.00% Mismatches: 100.00% Indels:
:	Gaps:
US-10-750-262	-2 (1-339) x US-09-780-669-878 (1-1195)
Qу 1	MetGluSerArgLysAspIleThrAsmGlmGluGluLeuTrpLysMetLysProArgArg 20
Db 66	ATGGAAAGCAGAAAAGACTACACAAACCAAGAAGTACTTTGGAAAATGAAGCCTAGGAGA 125
Оу 21	AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
Db 126	AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185
Оу 41	ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
Db 186	CCTGTGCTTTTGCACTTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245
0у 61	LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
Db 246	CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

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Sequence 878, Application US/09822827

; Sequence 878, Application US/09822827

; Patent No. US20020081680A1

; GENERAL INFORMATION:
   APPLICANT: Xu, Jiangchun
   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
   FILE REFERENCE: 210121.534C1

; CURRENT APPLICATION NUMBER: US/09/822,827

; CURRENT APPLICATION NUMBER: US/09/822,827

; CURRENT FILING DATE: 2001-03-28

; NUMBER OF SEQ ID NOS: 982

; SOFTWARE: FRSEUSEQ for Windows Version 3.0

; SEQ ID NO 878

; LENGTH: 1195
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US-09-822-827-878
; TYPE: DNA
; ORGANISM: Homo
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                              Ly8GlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal
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Alignment Scores:

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APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-895-793-878
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Publication No. US20020192763A1
GENERAL INFORMATION:
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: Carter, Darrick
Li, Samuel X.
Aljun
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                        ATAGCAT CTCTGA CTTTT CTTTACA CTCTTCTGA GGGA A GTA A TTCA CCCTTTA GCA A CT
                                                IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr
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Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
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Houghton, Raymond L.
Vinals de Bassols, Cárlota
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Hepler, William T.
Henderson, Robert A.
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Mitcham, Jennifer L.
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APPLICANT:
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                 APPLICANT:
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        Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
                                                                                                                                                        Day, Craig H. Vedvick, Thomas S. Carter, Darrick Li, Samuel X.
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Kalos, Michael D.
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APPLICANT: Vinals de Bassols, Carlota

APPLICANT: FOY, Teresa

APPLICANT: FOY, Teresa

APPLICANT: GATYR.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121. 427C26

CURRENT APPLICATION NUMBER: US/09/895,814

CURRENT FILING DATE: 2001-06-29

NUMBER OF SEQ ID NOS: 990

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 878

LENGTH: 1195

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Foy, Teresa
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                                     Percent Similarity:
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Query Match:
US-10-750-262-2 (1-339) x US-10-012-896-878 (1-1195)
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEC 17 NOC. 10.1
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APPLICANT:
APPLICANT:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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                                                                                                                                                TYPE: DNA
ORGANISM: Homo
                                                                                              No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stolk,
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Vedvick, Thomas S.
Carter, Darrick
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Kalos, Michael D.
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Hepler, William T.
Henderson, Robert A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harlocker,
                                                                                                                                                                                                                                                                                                                                                    McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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                              Length:
Matches:
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	966 GTCCTGATATTTAAAAGCATA 321 ArgHisGlyTrpGluAspVal'
DroThrPheMetIleAlaValPheLeuProIleVal 	281 Ly 006 AA
. GAGIGACICITIGACATGGAAGAATTTCACTATATTCAGAGCAAGCTÁGGAÁTTGTT FLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 	Oy 261 SerLeuLeuGlyThrileHisala
CTGGCTCTGTTGC PheHisTyrIleG	726 TO 241 Va
eLeuAlaLeuLeuAlaValThrSerIleProSer	221 Ser
IGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 	201 Glr 666 CAA
erTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 	81 Sea
ePhePheAlaValLeuHisAlaIleTyrSeTLeu 	161 Argly: 546 AGAAA
mGlyThřlyefyřířjelysPheProHisTrpLeuAspLysTrpMetLeuThr 	141 LeuHisAs 486 CTTCATAA
lTyrLeuProGlyValIleAlaAlaIleValGln TTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA	121 ValserI] 426 GTTTCCAT
rPheTyrLysIleProIleLeuVallleAsnLysValLeuProMet 	01 SerHisGlnGlnTy
::LeuinrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaTh: 	306 ATAGCATCTCTGAC
CACAGTGGCACTTGCCAATTAAAATAGCTGCTATT	246 CTTCAGCACACACAGGAACTCTTTC
roGlnTrpHisLeuProIleLysIleAlaAl	61 LeuGlnHisThrGlnGluLeuPheP
hrAlaHisAlaAspGluPheAspCysProSerGlu CAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA	41 ProValLeuLeuHisLeuHisGlnT
	AATTTAGAAGAAGACGATTATTTGO
ACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAC isLysAspThrGlyGluThrSerMetLeuLysAr	y 5 04 5021
MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgAr	Qy 1 MetGluSerArgLysAspIleThrA:

Search completed: December 6, 2005, 20:50:02 Job time : 959 secs

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Result a Database : -MODEL-frame+ p2n.model -DEV=xlh -Q=/cgn2 l/USPTO spool h/US10750262/runat_06122005 162948 15696/app query.fasta_1.519 -Q=/cgn2 l/USPTO spool h/US10750262/runat_06122005 162948 15696/app query.fasta_1.519 -DB=PublIshed_ApplicatIons_NA_New_QFNT=fastap -SUFFIX*=rnbn -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITG=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFNT=pc0 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -USER=US10750262 @CGN 1 1 120 @-runat 06122005 162948 15896 -NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB Maximum DB Total number of hits satisfying chosen parameters: Searched: OM protein - nucleic search, using frame_plus_p2n model Command_line parameters: Scoring table: Perfect score: Run on: ŏ Pred. No. score grea Score 107 99.5 99.5 93.5 93.5 92.5 90.5 90.5 d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution. seq length: seq length: Query Match Published_Applications_NA_New:* Xgapop 10.0 , y Ygapop 10.0 , y Fgapop 6.0 , I Delop 6.0 , I 3289935 seqs, 155610033 residues BLOSUM62 1 MESRKDITNQEELWKMKPRR.....IRHGWEDVTKINKTEICSQL 339 December 6, 2005, 16:29:58 ; Search time 159 Seconds (without alignments) US-10-750-262-2 //cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:* //cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:* //cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:* //cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:* //cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:* //cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:* //cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:* //cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:* //cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:* //cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:* //cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq3:* 20000 GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. Length 3137 2622 2803 819 3263 1179 1564 1515 2000000000 В 0 1 0 0 0 0 0 0 Xgapext Ygapext Fgapext Delext US-10-793-626-3842 US-10-750-185-48126 US-10-750-185-29256 US-10-793-626-1307 US-10-793-626-3595 US-10-793-626-3305 US-10-793-626-3305 US-11-110-977-1 US-10-467-657-2439 ID SUMMARIES 7.0 663.545 Million cell updates/sec 6579870 Sequence 3842, Ap Sequence 48126, A Sequence 29256, A Sequence 1307, Ap Sequence 3395, Ap Sequence 3305, Ap Sequence 1, Appli Sequence 2439, Ap Description

Alignment Pred. No.: Score: Percent Si Best Local Query Matcl	RESULT 1 US-10-793-626 Sequence 38 Publication GENERAL INF APPLICANT: TITLE OF 1 FILE REFER CURRENT FI CURRENT FI PRIOR APPL PRIOR APPL PRIOR APPL PRIOR OF SOFTWARE; SEQ ID NO 3; LENGTH: 3 TYPE: DNA ORGANISM: FEATURE; FEATURE; FOTHER INF OTHER INF		.4.	0 44 44	42	C 40		36 37	. W. I	33		c 29	28		C 24	22 23		c 19	17 18	c 16	-	c 12	o 11	
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Length: 3137 Matches: 64 Conservative: 55 Mismatches: 94 Indels: 58 Gaps: 17	0793626 OHN CCUS EPIDERMIDIS NUCLEIC (10/793,626 04 64,258 64,258 in of Artificial Sequence: id sequence	ALIGNMENTS	S-10-821-234-	-10-467-657-677	-10-750-185-3862 -11-174-150-17	10-750-185-45	-11-055-822-593 -10-793-626-416	-10-750-185-492 -11-055-822-507	10-793-626-1693	-10-485-517-51	-10-793-626-	-11-074-176-221 -10-793-626-370	-11-102-240- -11-068-686-	-10-467-657-	-10-793-626-	10-750-185 10-793-626-	-10-793-626- -10-793-626-	-10-793-626-	-11-074-176-237 -10-750-185-2634	-10-793-626-2205	S-10-750-185	10-793	-10-793-626	S-11-102-978
	ACIDS AND PROTEINS		Sequence 60435, A Sequence 193, App	quence 677	Sequence 38622, A Sequence 17, Appl	quence 450	900	equence 49215	equence 1458 equence 1693	equence 51	equence 3902	2 22 1	equence 77 equence 3.	Sequence 3523, Ap Sequence 7791, Ap	quence 4182,	Sequence 27964, A	quence 4281, quence 4070,	quence 3829,	equence	equence 3//6.	equence 366	nce 3381, A	equence 4225, equence 4209,	equence 3, Appl

US-10-750-262-2 (1-339)

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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOY
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
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                                                                                                                                                                           Sequence 48126, Application US/10750185 Publication No. US20050260603A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                        669
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                                                                                                                                                                                                                                                                            788 ATTGAAGAACTTTTATTTCGTCATTTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaThrSerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeu 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTCAAGGTCTAATATTÄGTTATCTTTÄTAAAATGCATCAATCTGTÄÄTÄAATGAATGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValGlnLeuHisAsnGlYThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMet 158
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                                                                                                                                                                                                                                                                                                                                                                    -----TrpTyrThrProProThrPheMet---IleAlaValPheLeuProIle 299
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; ORGANISM: Bovine
US-10-750-185-48126
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 48126
LENGTH: 2622
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Qy 31 AspThrGlyGluThrSerMetLeuLysArgProValLeuLeuHisGlnThrAla 50	Alignment Scores: Pred. No.: 99.50 Score: 99.50 Matches: 75 Percent Similarity: 34.15* Best Local Similarity: 20.33* Query Match: 6 Gaps: US-10-750-262-2 (1-339) x US-10-750-185-29256 (1-2803) Qy 17 LysProArgArgAsnLeuGluGluAspAspTyrLeuHisLys 18 Db 1251 AGGAAACAGAGAGAGAGGACCTAGAGGAGGATCTAATCAGCTCATGGAATGATTCCCTTAGA 1307	ANT: FANTIN OF INVENTION EFERENCE: MM T APPLICATION T FILING DATE APPLICATION P FILING DATE OF SEQ ID NO RE: PatentIN NO 29256 H: 2803 DNA ISM: BOVING ISM: BOVING INVENTED IN INC.	Qy 293IleAlaValPheLeuProIleValValLeuIlePheLysSerIleLeuPheLeuProC 312 Db 293IleAlaValPheLeuProIleValValLeuIlePheLysSerIleLeuPheLeuProC 312 Db 293 TGTCATCCCTGTTTATACCATTGTGGTGCCATGATCATATATA 2146 Qy 312 YSLeuArgLySLySIIELeuLyS 319 Db 2147 GTTTGAGGAACAAGGATGTCAAA 2169 RESULT 3 US-10-750-185-29256 Sequence 29256, Application US/10750185 PUBLICANT: NO. US20050260603A1 GENERAL INFORMATION: APPLICANT: DeNISS, Sue K. APPLICANT: DeNISS, Sue K. APPLICANT: DeNISS, Sue K. APPLICANT: MMI GENOMICS, INC. APPLICANT: HOLM, Tom APPLICANT: HOLM, Tom APPLICANT: HOLM, Tom APPLICANT: BATES, Stephen
US-10-793-626-1307 Sequence 1307, Application US/10793626 Publication No. US20050255478A1 GENERAL INFORMATION: APPLICANT: KIMMERLY, WILLIAM JOHN TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS FILE REFERENCE: PU3480US CURRENT APPLICATION NUMBER: US/10/793,626 CURRENT FILING DATE: 2004-03-04 PRIOR APPLICATION NUMBER: 60/164,258 PRIOR FILING DATE: 1999-11-09 NUMBER OF SEQ ID NOS: 4472 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1307 LENGTH: 819 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic US-10-793-626-1307	Qy 265GlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIleLysGln 282	210 1806 219 1866 239 1923 255	Db 1461 TTTGCAACTTTGTGGCAGAAAGCCTTCCTGCAGGAACTCATGGCTGACAGAATATATAA 1520 Qy 142 HisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThrArg 161 1521 TGTTCTGTTCGCAAG

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Sequence 3595, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
APPLICANT: KIMMERLY, WILLIAM JOHN
APPLICANT: KIMMERLY, WILLIAM JOHN
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; FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3595
LENGTH: 3263
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

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PRIOR FILING DATE: 1999-11-09 NUMBER OF SEQ IN MOST 4472 SOFTWARE: Patentin Ver. 2.1 SECTIMNAJOS S. 1.1 SECTIMNAJOS S. 1.1	Db 279 ABPILE
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286 GTGTTGAGTAAACAGACCAAGTTGGATCATGGGGAATTTCAGAGGTCATGCCCTCCCT	Db 2:	
0-262-2 134 V	US-10-750-2 Qy 1:	
Intent Scores:	Alignment S Pred. No.: Score: Percent Sim Best Local Query Match DB:	
FY: 1564 E: DNA ANISM: Homo Sapiens FURE: F/KEY: CDS ATION: (314)(1138) RR INFORMATION:	LENGT TYPE: TYPE: ORGAN FEATU NAME/ LOCAT OTHER 11-110	
CURRENT APPLICATION NUMBER: US/11/110,977 CURRENT FILING DATE: 2005-04-19 PRIOR APPLICATION NUMBER: US/10/112,645 PRIOR FILING DATE: 2002-03-28 PRIOR APPLICATION NUMBER: US 60/280,514 PRIOR APPLICATION NUMBER: US 60/280,514 PRIOR FILING DATE: 2001-03-29 PRIOR FILING DATE: 2001-03-29 NUMBER OF SEQ ID NOS: 9 SOFTWARE: Patentin version 3.1	CURRENT F CURRENT F PRIOR APP PRIOR APP PRIOR FIL PRIOR FIL NUMBER FIL NUMBER SOFTWARE:	
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256 LysLeuGlyIleValSerLeuLeuLeu 264 ::: ::::: ::::: 1111 TTGATAGGTTTAATTAGTCTTATCATT 1137	Db 04	
1087 GAATATGTTACTTATACTAGTGCA 1110	Db 43	
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US-10-750-262-2 (1-339) x US-10-467-657-2439 (1-1515)
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SegWin99, version 1.04
SEQ ID NO 2439
LENGTH: 1515
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2439, Application US/10467657 Publication No. US20050260581A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 APPLICANT: CHIRON SPA
APPLICANT: FONTANA MARIA RITA
APPLICANT: PIZZA MARIAGRAZIA
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND
FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nTrpHisLeuProlleLysIleAlaAlaIleIleAlaSerLeuThrPheLeuTyrThrLe 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        olleLeuVallleAsnLysValLeuProMetVal-----SerIleThrLeuLeuAlaLe 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nTrpAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTr 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCCAAGÁTTTÁCCACAGCGGCAAAGGCGTTGCCCGTCCTTÁTCCCCGTCÁÁÁACCCCTC--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pMetLeuThrArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAla--
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                                                                                                                                                                                                                                                                                                                                                             aLeuLeuAlaValThrSer-------IleProSerValSerAspSerLeuThrTr
                                                                                                                                                                                                                                                                                                                                                                                             pargMetGluIleTyrValSerLeuGlYIleVal------GlYLeuAlaIleLeuAl 231
                            TGCCTATTTCATGCTTTACCTGCCGATGGCGCAAACCACCCTGAGGACTTCCTTGGAACA 1211
                                                                                                                                                                                                             ATTATGTGCCTTGCCCCTTGTTTGGGCATCGGTTCGCTATCGCAATTTTTTAACCGTTTG
                                                                                                                                                                                                                                                                                                   pArgGluPheHisTyrileGlnSer---LysLeuGlyIleValSerLeuLeuLeuGlyTh
                                                                                                                                                                                                                                                                                                                                 GATGATGGTCGGCACTTCCGGGCACATTCGCGCTCGTATCCGTATTTGATGCC------
                                                                                                                                                                            pileAspIleLysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLe 297
                                                                                      uPro----
                                                                                                                                                 ĠĀŤĀĠĀĊAGGCTGCCGŤŤŤTTACTGCACGCCGTCĊĊĊGGTTTGGTTĀŤĊĠĊĊCTATCCTT
                                                          ePheLysSerIleLeuPheLeuPro----
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -------AAACTGCCCGGTCAGATCGGCGCGATTGTTTT
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-TTTATCCGTTCCTTAAGCGTATCGGCTTTAGGTGCGATTTTGACTAT 971
                                                             --CysLeuArqLysLysIleLeuLy 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ProGlyValIleAlaAl 137
                                                                                                                          -----IlevalvalLeuIl 303
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194

783

815

247 872

924

1091

1031

Pred. No.: 4.23e+04 Accore: 87.50 Percent Similarity: 87.54 Best Local Similarity: 22.994 Mismatches: 97 Query Match: 7 CysPro-SerGluLeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLy 96 STCCACTCCAGAATTTATTTTTTGACAATGTTTTTTTTGACACATTGTATTGATTG	1212 ACTCCCCAAAGGGATGGAACAGGTC 1236 Tig9	Oy 319 sileArgHisGlyTrpGluAspVal 327
RESULT 10 US-10-793-626-4225/c Sequence 4225, Application US/10793626 Publication No. US20050255478A1 GENERAL INFORMATION: APPLICANT: KIMMERLY, WILLIAM JOHN TITLE OF INVENTION STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS CURRENT APPLICATION NUMBER: US/10/793,626 CURRENT APPLICATION NUMBER: 60/164,258 PRIOR APPLICATION NUMBER: 60/164,258 PRIOR APPLICATION NUMBER: 60/164,258 PRIOR FILLING DATE: 1999-11-09 **NUMBER OF SEQ ID NOS: 4472 **SEQ ID NO 4225 **ID NO 4225 **ID NO 4225 **ID NO 4225 **OFTWARE: Patentin Ver. 2.1 **ORGANISM: Artificial Sequence FEATURE: **OTHER INFORMATION: nucleic acid sequence US-10-793-626-4225 **Alignment Scores: Pred. No.: **OTHER INFORMATION: nucleic acid sequence US-10-793-626-4225 **Alignment Scores: **Pred. No.: **OTHER INFORMATION: 37.9 **Pred. No.: **OFTWARE: B7.00 **Percent Similarity: 32.58* **Description of Artificial Sequence US-10-793-626-4225 **Alignment Scores: **OTHER INFORMATION: nucleic acid sequence US-10-793-626-4225 **Alignment Scores: **Alignment	Db 18425 TITTATACATICCTCATGGTTAGATTTTCAGGCTTAACTGGAATGATGGTTAGAGCTGGAATGAAGAGGCG 184294 Qy 162 sGlnheGlyLeuLeuSerPhePhePheAlaValLeuHisAlalleTysErLe 180 184295 GATTTAAAATTCTCTCTCTCTCTCTCTCTCTCTCGCACCATTCCTATTGTCT 184354 Qy 18295 GATTTAAAATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	

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US-10-750-262-2 (1-339) x US-10-793-626-4225 (1-3083)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 LeuLeuSerPhePhePheAlaValleuHisAlaIleTyr------------
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                                                                                                                                                                                                                                                                                                                                                                                                                          232 LeuLeuAlaValThrSerIleProSerValSerAspSerLeuThrTrpArgGluPheHis
321 gHisGlyTrpGluAspValThrLysIleAsnLysThr 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCACCATTTGCAGATATGGCAATTTTATTAGGTCTTAACTGGTTAGCAATATTACTTTAT 2824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuProIleLysIleAlaAlaIleIleAlaSerLeuThrPheLeuTyrThrLeuLeu---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProSerGluLeuGlnHisThrGlnGluLeuPheProGlnTrp-------His 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGTTACGCGCTATGGAAGAAAATGGGCATATTCCTAAATTCTTAGGTAAAATTAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrieuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGlnLeuHisAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTAGTTGCATATTTAACTGGTCCAACTACGGTTATTTCATTACGTAAAATGGCACCA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACATTGTTCCGTGACTGG------GGTACACTAGCTGCGGTTATTTCTACTGCAACA 2593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAGAAGTTATTTTAATTATTTTÄGGTTTACCTATTTATTTCTTCTATGAATATAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---TyrLysIleProIleLeuValIle-----AsnLysValLeuProMetValSerIle 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ArgGluValIleHisProLeuAlaThr-------
                                                                                                                                                                                                                                                                                                                                                                                   TICTTATCATTTATTGGAAGTAAAGAGTTCAAA---GGCTTAAATTGG-----ATTCAC 2251
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                                                                                                                                                                                                                                                                                                  TATCCATGGGATTTCTTAGTCATTGTAATCGTTGCTTTAATCTTCTATCAACTAGGTA--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspValTrpArgMetGluIleTyrValSerLeuGlyIleValGlyLeuAlaIleLeuAla
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                                                                                lLeuIlePheLysSerileLeuPheLeuProCysLeuArgLysLysIleLeuLysIleAr 321
                                                                                                                                                                                                                 TrpTyrThrProProThrPheMetIleAlaValPheLeuProIleValVa 301
                                             GCGATAAGTTGCGTAAAACACGCAAAAAAGCGCGTCATAAAGATTGG
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-AAAATGACTCCATTTAAAGCTAATATTTTAAAATTTATGGCA 249:
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Best Local Similarity:
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APPLICANT: KIMMERLY, WILLIAM JOHN
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: U5/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 607-64,258
PRIOR APPLICATION NUMBER: 607-64,258
PRIOR FILING DATE: 1999-11-09
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LENGTH: 3311
TYPE: DNA
ORGANISM: Artificial Sequence
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Publication No. US20050255478A1
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                                                                                                                                           2151 ATTTTTCCATCAGTCAAATGAAAAACACCATAAAGAAACAGGAGACGAACATCATTTCGA 2092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 sIleProIleLeuValIleAsnLysValLeuProMetValSerIleThrLeuLeuAlaLe 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuprolleLyslleAlaAlaIleIleAlaSerLeuThrPheLeuTyrThrLeuLeu-Ar
                                                                                                                                                                                                                                GATTCAAGCAGCAGGTGCTGTTTACTTAATCTATATGTCTATTAAA---AATTTAIGGCA 2152
                                                                                                                                                                                                                                                                                                                 TGCATTCATTTTAGATTTATTGCTTTATTTTTAATAAGTATTATTGCAAACTTCTGGTG 2205
                                                                                                                                                                                                                                                                                                                                                           rPhePhePheAlaValLeuHisAlaIleTyrSerLeuSer-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nTrpAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHis-----
                                                                                                                                                                                                                                                                                                                                                                                                    ACATCTACCACCTAAACAACGTAAAAAAAGCACTTTTTT----TATGGCCTATTAGG
                   lSerLeuGlyIleValGlyLeuAlaIle-----LeuAlaLeuLeuAlaVal---Th 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description of Artificial Sequence: synthetic nucleic acid sequence
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87.00
35.71%
22.79%
4.86%
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Matches:
Conservative:
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Indels:
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108 1215 128 1158 1158 148	Mismatches: 95 Indels: 94 Gaps: 13)-793-626-3381 (1-4071)	Description of Artificial Sequence nucleic acid sequence sequence 57.9 Length: 57.9 Matches: 35.71% Conservative:	OMBER: U 2004-03 BER: 60/ 99-11-09 4472 r. 2.1	IDERMIDIS NUC		Qy 236 rSerIleProSerValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLy 256
TH: DN VISM V-65 V-65 Simi Il Simi	APPLICANT: PIZZA MATIAGRANIA APPLICANT: MASIGNANI VEGA APPLICANT: MASIGNANI VEGA TITLE OF INVENTION: GONOCCCCAL PROTEINS AND NUCLEIC ACIDS FILE REFERENCE: CURRENT APPLICATION NUMBER: US/10/467,657 CURRENT FILING DATE: 2003-08-11 PRIOR APPLICATION NUMBER: GB-0103424.8 PRIOR FILING DATE: 2001-02-12 NUMBER OF SEQ ID NOS: 9218 SOFTWARE: SeqWin99, version 1.04 SEQ ID NO 4965	SULT 13 SULT 13 -10-467-657- Sequence 496 Publication Publication APPLICANT:	Qy 272	Qy 236 rSerIleProSerValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLy 256		1098 168 1047 182 987

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RESULT 14
US-10-185-36689
; Sequence 36689, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
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                                                                                                                                                                   964 GGCTTTGTCGGAATGTTGGCCGGATTGCCTTTGGCCGCCGTAACCTTGGTCTTGCTTCGC 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         703 GATTCGGGATTTGCCATCGGTATGGTTGCCGGTATTTTGGTGTTTTGTCCCCTAT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGAACACGCTGCTGCCGTGGTTGAAAAATACAATCGGCGGATATGTGGAAATCGATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MetGluIleTyrValSerLeuGlyIleVal------GlyLeuAlaIleLeuAlaLeu
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                                                                                                                                     HisGly 323
                                                                                                                                                                                                                                      CGTATCGGCCTGTCGCCGTTTTGGGTTATCTTTTCGCTGATGGCGTTCGGAGAGCTGATG 963
                                                                                                                                                                                                                                                                                                        GTTTTTGCCGTCGGTCAGTTTCTCGAAAGTTTTTTCATTACGCCGAAAATTGTAGGAGAC 903
                                                                                                                                                                                                                                                                                                                                      ThrPheMetIleAlaValPheLeu-------ProIleValVal-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                         -TTGGGTGCGTTTACGGGATTGCTGCTTGCCACTGTTGCAGCCTTGCTC
                                                                                                                                                                                                                                                                         -----LeuilePheLysSerIleLeuPhe-------
                                                                                                                                                                                                     ----LeuProCysLeuArgLysLysIleLeuLysIleArg 321
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: NMIL1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
VUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 36689
LENGTH: 1138
TYPE: DNA
ORGANISM: Bovine 19866880906331
US-10-750-185-36689
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                                                                                                                                                                                                                                                                                                                                      349
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                                                                                                                                   472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 LeuLysArgProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCys
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ROSENFELD, David
HOLM, Tom
BATES, Stephen
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                                                                                                                                                                                                                                                                    CAAGATGGTAATAATCTTATCTATAATGAGTTTCTCTATAGGAGATTCACTGGCATAGAG 447
                                                                                                                                                                                                                                                                                                HisAsnGlyThrLys--------TyrLysLysPhe-----
                                                                                                                                                                                                                                                                                                                                    SerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGlnLeu 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCATCAAGACTCTTGTG-------TTTATAGATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheLeuTyrThrLeuLeuArgGluVallleHisProLeuAlaThrSerHisGlnGlnTyr 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ileAlaAlaIleIleAlaSerLeuThr 85
                                                                                                                                                                 LeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeuSerTyrProMetArgArg 186
                                                                                                                                                                                                                                                                                                                                                                                                    TTTGGCAAAGCATAGATTTTATTTTTGGACTTGTTTTTCCAATGCTCTTTCTCCTAATATT
                                                                                                                                  |||:::|||
|----TTTTGGTTTTGTTTTGTTCTTTCTATATTCTCCTGAGTTCTAACATATCACGCT 525
                                                                                                                                                                                                     TTGACACTCAATCCATCGTGGCTT---
                                                                                                                                                                                                                                 ------ProHisTrpLeuAspLysTrpMetLeuThrArgLysGlnPheGlyLeu 166
                                                                 TCAGTAAGATATAAAATATATGCATAGCTGGTAGAAAGACACTTTCAAGATACAGTTTCA 585
                                                                                        ---AlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHisAs 212 ::::::
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85.50
36.34%
20.42%
4.78%
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Matches:
Conservative:
Mismatches:
Indels:
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471

195

Qy 164
99 11 12 12 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13

Search completed: December 6, 2005, 18:50:55 Job time : 320 secs

Pilo Paga Orang Caralan

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Result
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-MODEL-frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_epool h/US10750262/runat_06122005_162946_15642/app_query.fasta_1.519
-O=/cgn2_1/USPTO_epool h/US10750262/runat_06122005_162946_15642/app_query.fasta_1.519
-DB=Issued_Patents_NA -OPMT-fastap -SUPFIX=rni -MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10750262_@CGN_1 1 193 @runat_06122005_162946_15642 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - nucleic search, using
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                                                                                                                                                                                                                                                                                                                     and is
          1358.5
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PE_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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length: 2000000000
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Ygapop 10.0 , Ygapext
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1790
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                                                                                                                                                                                                            Length
          ВВ
    US-09-455-486-1

US-09-333-873A-1

US-09-685-166A-878

US-09-679-426-878

US-09-759-143-878

US-09-759-143-878

US-10-010-667A-1

US-10-012-896-878

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US-09-323-873A-6
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ALIGNMENTS

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Percent Similarity:
Best Local Similarity:
                                                           Pred. No.:
                                                                               Alignment Scores:
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APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SEPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.17-US-I1
CURRENT ETLING DATE: 1999-12-06
CURRENT ETLING DATE: 1999-12-06
CURRENT FILING DATE: 1999-12-06
CURRENT ETLING DATE: 1991-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application Patent No. 6833438 GENERAL INFORMATION:
                                                                                                                                                                                                                  LENGTH: 11
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/323,873 PRIOR FILING DATE: 1999-06-01
                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                           ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                         NAME/KEY: CDS
                                                                                                                                        LOCATION:
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              Length:
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Query DB:

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APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANTO: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO:
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO:
TITLE OF INVENTION NUMBER: US/09/323,873A
CURRENT APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-323-873A-1
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LENGTH: 1195
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APPLICANT: Witcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Us, Craig H.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Welser, Milliam
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION NUMBER: US/09/685,166A
CURRENT APPLICATION UMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-685-166A-878
 Percent Similarity:
Best Local Similarity:
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US-09-685-166A-878
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                  ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu
                                                          GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT
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APPLICANT: Skelky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 20121.427C20

CURRENT APPLICATION NUMBER: US/09/679,426

CURRENT FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 895

SOFTWARRE: PastSEQ for Windows Version 3.0

SEQ ID NO 878

LENGTH: 1195
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; Sequence 878, Application US/09679426
; Patent No. 6759515
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; ORGANISM: Homo sapiens
US-09-679-426-878
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Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
Mitcham, Jennifer L.
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APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William
ITILE OF INVENTION: COMPOSITIONS AND METHOD
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE C
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
NUMBER OF SEG ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
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Patent No. 6800746
GENERAL INFORMATION:
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LENGTH: 1195
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ORGANISM: Homo:
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Vedvick, Thomas (
Carter, Darrick
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Henderson, Robe
Kalos, Michael
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Mitcham, Jennifer L.
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       ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
                                                              LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal
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                                                                                                              TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT
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APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene S.
APPLICANT: Hobert, Rene S.
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Saffran, Douglas C.
FILE REFERENCE: 511582001601
CURRENT APPLICATION NUMBER: US/10/010,667A
CURRENT APPLICATION NUMBER: 09/323,873
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
INMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 1195
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ORGANISM: Homo
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ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
                                                                         SerHisGlnGlnTyrPheTyrLysIleProIleLeuVallIeAsnLysValLeuProMet
                                                                                                                                             IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluVallleHisProLeuAlaThr
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                                                   TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
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Patent No. 6943236
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Boy, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Day, Craig H.
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  T: Foy, Teresa
T: Fanger, Gary R.
T: Wantanabe, Yoshihiro
T: Meagher, Madeleine Joy
INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
INVENTION: DIAGNOSIS OF PROSTATE CANCER
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                                                                                                            Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
                                                                 Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                                                               Day, Craig H.
Vedvick, Thomas
Carter, Darrick
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CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                     LeuHisAsnGlyThrLysTyrLysLysLysPheProHisTrpLeuAspLysTrpMetLeuThr
                                                                                                                                                                                                                                                 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
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                                                                                                                                                                                                                                                                                                                                                    | SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal
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                                                                                       | GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal
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APPLICANT: VENTER, J. CTAIG et al.
APPLICANT: VENTER, J. CTAIG et al.
APPLICANT: VENTER, J. CTAIG et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
A. PRIOR, APPLICATION NUMBER: 60/241,755
PRIOR, APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-20
PRIOR PRIOR DATE: 2000-10-03
PRIOR PRIOR DATE: 2000-10-03
PRIOR PRIOR DATE: 2000-09-09
PRIOR PRIOR DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PRIOR DATE: 2000-09-09
PRIOR PRIOR DATE: 2000-09-09
PRIOR PRIOR DATE: 2000-09-09
PRIOR PRIOR DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2686
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US-09-949-016-2686
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LENGTH: 1147
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                                                                                                                                                                                                                CTGTGCTTTTGCATTTGCAGCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA
                                                                                                                                               CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
                                                                                                                                                                    LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysIleAlaAlaIle
                                                                                                                                                                                                                                                                                AATTTAGAAGAACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA
                                                                                                                                                                                                                                   ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu
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GENERAL INCOGRATION:
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NUMBER: US/09/323,873A
CURRENT APPLICATION NUMBER: 60/087,520
FRICR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 3627
TYPE: DNA
CRANISM: Homo Sapiens
US-09-323-873A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ly8GlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal
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	241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIle
	6 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACA
	erLeuGlyIleValGlyLeuAlaIleLeuAl
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	181 SerTyrProMetArgArgSerTyrArgTyrIy8LeuLeuAsmirpAlaiyYGLIW
	raatggaacc
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	70 ValserTleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAl
	01 SerHisGlnGlnTyrPheTyrLysIleProIleLeuVallIleAsnLy
	TAGCATCTCTGAGGGAAGTAATTCA
	zrLeuThrPheLeuTyrThrLeuLeuArgGluValIleH
Db 1295 CCCTTCAGAA 275	
	euGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysI
sProSerGlu 60	ProValLeuLeuHisGeuHisGlnThrAlaHisAlaAspGluPheAspC\
raaaaaga 215	AGAAGAAGACGATTATTTGCATAAGGACACCGGGAGAGACCCA
rmetleulysarg 40 Db 1235 AGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTAGTAGA	uGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSe
GCCTAGGAGA 1	AATG
BProArgArg 20	MetGluSerArgLysAsplleThrAsnGlnGluGluLeuTrpLysMetLy
253	0-750-262-2 (1-339) x US-09-323-873A-6 (1-3627)
Db 1115 GTTTGTTTTTTTGAGATGAAGTCTCGCTCTGTTGCCCCATGCTGGAGTACAGTGGCACGAT	: 75.89% Indels: 3 Gaps:
253	Similarity: 29.68% Conservative: 0
Db 1055 TAAAAGGCATTAAAATATTCTTTGTTTTTTTTTTTTTTT	1.17e-150 Length: 1358.50 Matches:
253	Scores:

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3155 CATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAGATGAGGTAGGATGGGATAAACT 3214	253		3035 ATTTTGTTCACTTAGACAGCTTGGAGACAAGAAATTACCCCAAAAGTAAGGTGAGGAGGAT 3094	2975 AAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAG		2915 AATTAAGACAAATACACAAGAGACAAAGCACAAAAAAATAAAT	2855 GCAGTGATCCTGCTATAAGTAAGACTCAGTCCCTGATTTTAGGTATCCTGTGAAAAGCAG 2914	253 253	2795 TCTTCAATCTACCTATATTTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCT 2854	2735 CACATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAA 2794 253		2675 TTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCATTTATCAAAAATCAGAGTGAAT 2734	253 253	2615 TTTGTGCAGACATTGAAAAATTGTTCATATTATTTCCATGTTATCAGAATATTTGATTT 2674	253 253	2555 TAGTGACAAAGCATCCCAATGCAGGCTGAAATGTTTCATCACATCTCTGGATCTCTCTAT 2614	253	2495 TGTCAGAACACCGTTGAGATTACATAGGTGAACAACTATTTTTAAGCAACTTTATTTGTG 2554	253 253	2435 CAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGT 2494	253	2375 GATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCTGG 2434		2315 ACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAAACGCAAACTTAGCTATTT 2374		2255 CAACCAATGACATGTATTTTTCAACTAGTAACCTAGAAATGTTTCACTTAAAATCTGAGA 2314		2195 TATATGTACAATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAAACTAATTTT 2254	2135 CTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTAC 2194	253 253
QY 81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100		Db 216 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 275	156 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA	21 AsnL	Db 96 ATGGAAAGCARGAAAAACACATCACAAAAACAAAACAAACAACAACAACAAC	-10-750-262-2 (1	75.89%	Conservative:	nt Scores:		A 27	FastSEQ for	SEQ ID NOS:	CURRENT FILING DATE: 1099-12-06; PRIOR APPLICATION NUMBER: 09/323,873	INCE: 129.17-US-II	TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF	APPLICANT: Douglas C. Saffran	APPLICANT: Rene S. Hubert APPLICANT: Arthur B. Raitano	FORMAT	; Sequence 4, Application US/09455486 ; Patent No. 6833438	RESULT 10	Db 3455 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 3511	Qy 321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339	Db 3395 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 3454	Qy 301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320	Db 3335 AAACAATTTGTATGGTATACACCTCCAACTTTATGATAGCTGTTTTCCTTCC	Qy 281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300	Db 3275 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATATA 3334		Qy 254 25nSerLysLeuGlylleVal 260

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	1415 TTCTAATATTTGAAACTTGTTAGACAATTTGCTACCCATCTAATGTGATATTTTAGGAAT 1474
2495 TGTCAGAACACCGTTGAGATTACATAGGTGAACAACTATTTTTAAGCAACTTTATTTGTG	253 253 Db
253	1355 CACCTCGGCCTCCCAAAGTGCTGGGATGACAGTTGTGAGCCACCACCACCTCAGCCTGCTCT 1414 Qy
2435 CAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAAGAGGTGT	253 253 იხ
253	1295 GACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCC 1354 Qy
2375 GATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCTGG	253 253 pb
253	1 10
2315 ACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAAACGCAAACTTAGCTATTT	N
253	N
2255 CAACCAATGACATGTATTTTCAACTAGTAACCTAGAAATGTTTCACTTAAAATCTGAGA	253
253	1115 GTTTGTTTTTTGAGATGAAGTCTCGCTCTGTTGCCCCATGCTGGAGTACAGTGGCACGAT 1174 Qy
2195 TATATGTACAATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAAACTAATTTT	
253	1055 TAAAAGGCATTAAAATATTCTTTGTTTTTTTTTTTTTTGTTTG
2135 CTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTAC	1 1 2
253	995 GTGCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCCTAGACATAAA 1054 Qy
2075 TGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGATGAACA	253
253	935 CATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATTAATAAT 994 Qy
2015 CAACATTCTCACAGAATTTCCTAATTTTGTAGGTTCAGCCTGATAACCACTGGAGTTCTT	N
253	875 TAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGATATAGAATATGTTGACTTTTACCC 934 QY
1955 CTGATTAGTTTGGAAAGTATGCCTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTA	
253	
1895 GACATTCGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCAT	241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIle
253	81
1835 TCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCA	240
253	755
1775 GTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAATTTAATTCAG	201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
253	695
1715 ACTATCTCAGATTTACTGAGGTTTATCTTCTGGTGGTAGATTATCCATAAGAAGAGTGAT	200
253	635
1655 CCAGCTTACATTTTATATACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAA	161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
253	516 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGG
1595 AATAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTT	141 LeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
253	515
1535 AGTAATGCCTTTTATGTTACACAACTTAGCACTTTCCAGAAACAAAAACTCTCTCCTTGA	121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140 Db
	TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 455
7	SerHisGlnGlnTyrPheTyrLyslleProIleLeuVallleAsnLysValLeuProMet 120
253	336 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACT 395

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; Sequence 6, Application US/10010667A
Patent No. 6887975
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
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                                                                                                                                                                                                                                                                                 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal
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Best Local Similarity:
Query Match:
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3627
TYPE: DNA
ORGANISM: Homo :
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PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Saffran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 511582001601
CURRENT APPLICATION NUMBER: US/10/010,667A
CURRENT FILING DATE: 2001-12-06
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            GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal
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                                                                                  SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal
                                                                                                                                                    ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu
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                                                                TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC
                                                                                                                               IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisDroLeuAlaThr
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Matches:
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17.4 min 17.4 min 18.68	Score: 1071.50 Matches: 309 Percent Similarity: 23.59% Conservative: 0 Best Local Similarity: 23.59% Mismatches: 2 Query Match: 59.86% Indels: 1000 DB: 3 Gaps: 2	PRGANIAM: Human 9-949-016-14428 ment Scores:	FastSE(14428 9073	PRIOR PILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012		CURRENT APPLICATION NUMBER: US/09/949,016 CURRENT FILING DATE: 2000-04-14. PRIOR APPLICATION NUMBER: 60/24/555	; APPLICANT: VENTER, J. Craig et al. ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF	ESULT 12 IS-09-949-01 Sequence 1 Patent No. GENERAL IN	w	GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT	Ob 3335 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	281 LysGlnPheValTrpTyThrProProThrPheMetIleAlav	261 SerLeuLeuGlyThrlleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280	Qy 254	315	Db 3095 AGGCAAAAAGAGCAGAAAGATGTGAATGGACATTGTTGAGAAAATGTGATAGGAAAACAAT 3154	Qy 253 253	253 253	Db 2975 AAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAG	253
4068 AGTAGGCACAGGGAAGAGTGTAGAAGGAGATTCACATTCAGGAAATAACTGTTGTTTGCA 4127	200 2 4008 ATGCAAAAAAAAAAAAAAAAAGTCATAAATTTGTGGAGACCTGTTATCAGGGCTTCAT 4 200 2		QY 200 200 Db 3888 CATGCACATTACAGTTCTATCCAAGTAAACCATCAAATAATTATTAGAAAATTAATAGAT 3947	QY 200 200 Db 3828 CTACCACCCTCACAAGATTACTTTTAATATTGTTGTTCTTCTCCTTGTTTACCAATATG 3887	3768 GGTACAACTTTAGCAACATAAGAAACATTTTGTTCATGGACGAGGCCATATTTCAAACTT 3		Qy 200 200	CTAATAAAAAGTCTAAGTCACCTAACAAATTAATCATTTCTCATTGTAATATCAATACCC	Db 3529 ĀĠĀTĀĊĀĀĠŦŤĠĊŦĀĀĀĊŦĠĠĠĊĀŤĀŤĊĀĀĊĀĠGT-AAGATGACAGTGTTGACACTGTTA 3587 Qy 200 200	189		Oy 149 LysPheProHisTrpLeuAspLysTrpMetLeuThrArgLysGlnPheGlyLeuLeuSer 168	Db 3349 GTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAAACTTCATAATGGAACCAAGTATAAG 3408	ATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTG	Db 3229 ACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCCATCAACATATTTTTTTT	Qy 89 ThrLeuLeuArgGluVallleHisProLeuAlaThrSerHisGlnGlnTyrPheTyrLys 108	Qy 69 ProGlnTrpHisLeuProIleLysIleAlaAlaIleIleAlaSerLeuThrPheLeuTyr 88	<u>3</u> 1	049 CATANGGANGGANGGANGANGGANGGANGANAAAAAGANGCTTGTTTTTGTATTTTGCANGCAA 49 ThralahigalaangGangdangcangcangcangcangcangcangcangcangcangc	US-10-750-262-2 (1-339) x US-09-949-016-14428 (1-9073) Qy

5148 TGAAGTTTCTAAATATTCTTGTAATTTTAAAACTATCTCAGATTTACTGAGGTTTATCTT 5207	, ,	5088 TTCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATATACTTACT		5028 CACTTTCCAGAAACAAAAACTCTCTCCTTGAAATAATAGAGTTTTTATCTACCAAAGATA 5087		4968 AAAAATATTCTTTTACCTGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACTTAG 5027	1 N	n w		دا ز	N	4788 GTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCCAAAGTGCTGGGATGA 4847		1728 ATGTCCAGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTTCCCATGTTGGCCAGGCTG 4787		4668 GTTCAGGCGATTCTCTTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACC 4727	253	,608 TGTTGCCCATGCTGGAGTACAGTGGCACGATCTCGGCTCACTGCAACCTGCGCCTCCTGG 4667	. 2	548 TTTTTTTTGTTTGTTTTTTTTGTTTGTTTGTTTTTTTGAGATGAAGTCTCGCTC 4607		488 TCTAATTAGGACAAGIGTTTCCTAGACATAAATAAAAGGCATTAAAATATTCTTTGTTTT 4547	25	428 GCAAAGATCTTATACTTGTTCCAATTAATGATGCTCCTCCTGTTGTTTTCCCTATTGCT 4487	253 253	368 TGTTTATGATATAGAATATGTTGACTTTACCCCATAAAAAAATAACAAATGTTTTTCAACA 4427	ω		8 CTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGTGTG	230 LeuAlaLeuLeuAlaValThrSerIlleProSerValSerBalSerLeuThrTrpArgGlu 249	210 GluHisAspValTrpArgMetGluIleTyrValSerLeuGlyIleValGlyLeuAlaIle 229		201
Qy 253 253	Db 6228 ATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATATTTAATTGAGAA 6287		Db 6168 TCATTATTCATTTATCAAAATCAGAGTGAATCACATTAGTCGCCTTCACAACTGATAAAG 6227		6108 ATTATTTCCATGTTATCAGAATATTTGATTTTTAAAAACATAGGCCAAGTTCATTCA		Db 6048 AATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTCAT 6107	Qy 253	Db 5988 GAACAACTATTTTTAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGA 6047	Qy 253	Db 5928 ATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGTTGAGATTACATAGGT 5987	Qу 253 253	Db 5868 CCTGAATAATTGTGAGTTCGATTTGTTCTGGCAGGCTAATGACCATTTCCAGTAAAGTGA 5927	Qy 253 253	Db 5808 TTCATATATGAAAACGCAAACTTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCG 5867	Qy 253 253	Db 5748 AACCTAGAAATGTTTCACTTAAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGA 5807		Db 5688 TATACAATACACATTTGGTAAAACTAATTTTCAACCAATGACATGTATTTTCAACTAGT 5747		Db 5628 GACTGCATCTTGACAACTGAGCCTATTCTACTATATGTACAATACCTAGCCCATAATAGG 5687	Qy 253 253	Db 5568 ATTGCTCTGCCTGTTACACATATGATGAACACTGCTTTTTAGACTTCATTAGGAATTTAG 5627	Qy 253 253	Db 5508 TAGGTTCAGCCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACAC 5567	253	e i	5388 CACACGIAIACICCANCACIIIII	253	5328 G	Db 5268 GACAAGATTCAAAGGACTAAATTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGG 5327	253	Db 5208 CTGGTGGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGTCT 5267

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APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
ITITE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 592
TYPE: DNA
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                                                                                                                                                                                                                                                                               APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Hitcham, Jennifer
APPLICANT: Harlocker, Susan
APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
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GENERAL INFORMATION: 71 150 3:00
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Patent No. 6329505
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Reed, Steven G.
Kalos, Michael
Fanger, Gary
Retter, Mark
Solk, John
Day, Craig
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                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 342
LENGTH: 592
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-342
                       Alignment Scores:
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; Sequence 342, Application US/09352616A
; Patent No. 6395278
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Best Local Similarity:
Query Match:
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                                                                                                                                                                        APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: XI, Jiangchui
APPLICANT: XI, Jiangchui
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR U
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT APPLICATION NUMBER: US/09/352,616A
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                                                                                                                                                      FastSEQ for Windows Version 3.0
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Indels:
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US-09-636-215-342/c
; Sequence 342, Application US/09636215
; Sequence 3620922
; Sequence 3620922
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
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Kalos, Michael D.
Ranger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
Mitcham, Jennifer L.
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1: /cgn2_6/ptodata/2/pubpna/US09

2: /cgn2_6/ptodata/2/pubpna/US07

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6: /cgn2_6/ptodata/2/pubpna/US10

7: /cgn2_6/ptodata/2/pubpna/US11

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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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Sequence 3, Appli
Sequence 547, App
Sequence 54184, A
Sequence 27, Appl
Sequence 54772, A
Sequence 64012, A
Sequence 64012, A
Sequence 62619, A
Sequence 46704, A
Sequence 52619, A
Sequence 52619, A
Sequence 57153, A
Sequence 57153, A
Sequence 57153, A
Sequence 57153, A
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Sequence 39315, A
Sequence 49060, A
Sequence 54610, A
Sequence 33875, A
Sequence 31880, A
Sequence 142, App
Sequence 48714, A
Sequence 38532, A
Sequence 31533, A
Sequence 31533, A
Sequence 31, Appli
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US-10-750-185-48072	US-10-750-185-30138	US-10-750-185-63586	US-10-750-185-54609	US-11-112-908-47	US-11-112-908-49	US-10-793-626-4262	US-10-750-185-27481	US-10-750-185-26752	US-10-750-185-44414	US-10-750-185-1485	US-11-112-908-46	US-11-145-703-176	US-11-145-703-175	US-10-750-185-52241	US-10-750-185-39246	US-10-750-185-38045	US-10-793-626-4023	US-10-793-626-4179	US-10-750-185-47856	US-10-793-626-3360	US-10-793-626-3478
Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
48072, A	30138, A	63586, A	54609, A	47, Appl	49, Appl	4262, Ap	27481, A	26752, A	44414, A	1485, Ap	46, Appl	176, App	175, App	52241, A	39246, A	38045, A	4023, Ap	•	47856, A	3360, Ap	3478, Ap

ALIGNMENTS

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Sequence 25365, Application US/10750185

| Publication No. US20050260603A1 |
| GENERAL INFORMATION: |
| APPLICANT: MMI GENOMICS, INC. |
| APPLICANT: MMI GENOMICS, Sue K. |
| APPLICANT: KERR, Richard |
| APPLICANT: HOLM, Tom |
| APPLICANT: HOLM, Tom |
| APPLICANT: HOLM, Tom |
| APPLICANT: HATES, Stephen |
| APPLICANT: BATES, Stephen |
| APPLICANT: FANTIN, Dennis |
| TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS |
| FILE REFERENCE: MMI1100-2 |
| CURRENT FILING DATE: 2003-12-31 |
| PRIOR APPLICATION NUMBER: US/10/750,185 |
| CURRENT FILING DATE: 2003-12-31 |
| PRIOR APPLICATION NUMBER: US 60/437,482 |
| PRIOR APPLICATION SEQUENCE: 12-31 |
| PRIOR APPLICATION NUMBER: US 60/437,482 |
| PRIOR APPLICATION SEQUENCE: 12-31 |
| PRIOR APPLICATION NUMBER: US 60/437,482 |
| PRIOR APPLICATION SEQUENCE: 12-31 |
| PRIOR APPLICATION NUMBER: US 60/437,482 |
| PRIOR APPLICATION SEQUENCE: 12-31 |
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; ORGANISM: Bovine 19866880604913
US-10-750-185-25365
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US-10-750-185-25365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 3.9%; Score 39.2; Di
Local Similarity 54.1%; Pred. No. 0.1;
les 80; Conservative 0; Mismatches
885 TAACTTATATTTTAAAAAACAATGTTGT 912
                                                                                        824 ATAAGTGGATAGATATAAAACAATTTGT 851
                                                                                                                                                                                                 825 AAAAGCACATGACACTTAGTCTTTTGCTGTGCAAATAAGATAAAATGATTTGTCCTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                   765 TGACATTAATTCTGTCTGTTACTGTTACTTGTATCGGGTTTAATTATATCATTA
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RESULT 2 US-10-750-185-39315/c ; Sequence 39315, Application US/10750185

GENERAL INFORMATION:

APPLICANT: MMI GENOMICS, INC. APPLICANT: DeNISE, Sue K.

Publication No. US20050260603A1

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David

Leplicant: BATES, Stephen

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
FRIOR FILING DATE: 2003-12-31
VARIES PRIOR APPLICATION NUMBER: US 60/437,482
FRIOR FILING DATE: 2003-12-31
VARIES PRIOR APPLICATION NUMBER: US 60/437,482
FRIOR FILING DATE: 2003-12-31
VARIES PRIOR SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 49060
LENGTH: 872
TYPE: DNA
ORGANISM
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                                                                           Matches
                                                                                                             Query Match
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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1688 AACAGCAAGCATGAAATTTGTTCTTCCTTGTCCTATTAATAGTTAAGAAGAACAAAGA 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1748 AGAGAAAGGGAAAATTCTGGAATATAAAATGCCATTCTGCAGTATATCTGCAGTCTCAAT 1689
                                 316 TTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              954 GAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCC 1011
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 TATTCTCTTATCCACAACCCCACCACCTCCAAACTCTTTCCCATATTTATTTTCATTGGG 116
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                                                                           Conservative
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                                                                                         3.5%;
                                                                     Score 36; DB 6
Pred. No. 0.61;
0; Mismatches
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Pred. No. 0.48;
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                                                                                                             DB 6; Length 872;
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US-10-750-185-63875/c
; Sequence 63875, Application US/10750185
; Publication No. US20050260603A1
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                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIN version 3.1
SEQ ID NO 54610
LENGTH: 1012
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMII100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION UNMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
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Best Local Similarity
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILIOOPER: US/10/750,185
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/437,482 PRIOR FILING DATE: 2002-12-31
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            355 CCAATGG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 AAAAATTTAGATGAATTATATTTTGTAAGAGTTTCACTTAAGGAGATAAAAAAAGAGCATC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 GCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTG 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAAATAAACCACCACAACATTTCTTTTATACTTCAGTTAGAGTGTTACATTGACTTTTT 296
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KERR, Richard
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US-10-821-234-142
US-10-821-234-142
; Sequence 142, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
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; ORGANISM: Bovine
US-10-750-185-30880
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US-10-750-185-30880
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; ORGANISM: Bovine
US-10-750-185-63875
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Best Local Similarity
Matches 106; Conserv
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SOFTWARE: PatentIN version 3.1
SEQ ID NO 30880
LENGTH: 1240
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Best Local Similarity
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INPERRING BOVINE TRAITS
FILE REFERENCE: MMILION-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
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APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/437,482 PRIOR FILING DATE: 2002-12-31
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                 Labat,
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                                                                                                                                                                                                                                                                           CATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCC 304
                                                                                                                                                                                                                                                                                                                AGCCCACCAGGCTCCCATCCTACTTTGCTACTTCCCCAGAATTAAGCTATAGCACAGAA 420
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                                                                                                                                                                                                                                                                                                                                                                                       TGCTGTTGCTGCTGAAGTTCTTCAGTCGTGTCTGACTCTGTGCGACCCCATAGACTGC 360
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                                                                                                                                                                                                ATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGT 350
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Stache-Crain, Birgit
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Pred. No. 4.5;
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SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 142
LEMOTTU
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT PAPPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR RILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: Patentin version 3.1
SEQ ID NO 46714
                                                                                                                         Matches
                                                                                                                                         Query Match
Best Local
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Publication No. US20050260603A1
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Best Local Similarity 47.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MMI GENOMICS,
APPLICANT: DENISE, Sue F
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TANG, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
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ORGANISM: Homo sapiens
                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Bovine
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                                                                                                                         79;
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DeNISE, Sue K.
KERR, Richard
ROSENFELD, David
HOLM, Tom
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                                                                                                                       Conservative
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                                                                                                                                       Score 33.8;
Pred. No. 5;
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Pred. No. 3.6;
0; Mismatches 117; Indels
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US-10-750-185-35293
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US-10-750-185-35293
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                                                                                                   SOFTWARE: PatentIN version 3.1 SEQ ID NO 35293
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35293, Application US/10750185
Publication No. US20050260603A1
Query Match
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Best Local Similarity
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SEQ ID NO 38532
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                                                                                                                                             APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE
FILE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE
FILE OF INVENTION OF INFERRING BOVINE
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                           APPLICANT:
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APPLICANT: FANTIN, Dennis
TITLE OP INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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                                                                                                                                    NUMBER OF SEQ ID NOS: 64922
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                                               TYPE: DNA
ORGANISM: Bovine
                                                                                   LENGTH: 973
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HOLM, Tom
BATES, Stephen
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KERR, Richard
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3.3%;
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Score 33.2;
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Pred. No. 5.3;
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DB
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Length 973;
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RESULT 12
US-11-108-172-547/c
; Sequence 547, Application US/11108172
; Publication No. US20050260177A1
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; LOCATION: (216732)..(216833)
; OTHER INFORMATION: C21orf34 exon
US-11-102-978-3
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US-11-102-978-3/c
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APPLICANT: University of Utah Technology Transfer Office
APPLICANT: University of Utah Research Foundation
TITLE OF INVENTION: Diagnosis and Treatment of Herpes Simplex Virus Disease
FILE REFERENCE: 0274-5537.1US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/11102978 Publication No. US20050250142A1
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CURRENT FILING DATE: 2005-04-11
PRIOR APPLICATION NUMBER: PCT/US2003/033152
PRIOR FILING DATE: 2003-10-18
PRIOR APPLICATION NUMBER: 60/419,576
PRIOR FILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 13
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LOCATION: (167308)..(167438)
COCATION: C167308: C210xf34 exon
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LOCATION: (80006)..(81)
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LOCATION: (56948)..(57115)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                           9548
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                                                                                                                                                                                                                                                                                    9668 AATTAAGATATCATAGGTTCAAGTTACACAATTTACACCTTTTATTGGTCATAAGTCACA
                                                                                                                                                              866 CAACTITTATGATAGCTGTTTT 887
                                                                                                                                                                                                                                                                                                                  746 AATTTCACTATATTCAGAGCAAGCTAGGAATTGTTTCCCTTCTACTGGGCACAATACACG
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                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                     CAGTAGCATATTTTATTTGTCATTTAATTGATTCAAAACCAAAAATATATGTTACCCCTT 9549
                                                                                                                                                                                                                                           CATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTGTATGGTATACACCTC 865
                                                                                                                         CTATTGCTAAGCCAGGTATTAT 9527
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                                                                                                                                                                                                                                                                                                                                                                               Score 33.2;
Pred. No. 98;
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0; Mismatches
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GENERAL INFORMATION:

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RESULT 13
US-10-750-185-58068
US-10-750-185-58068, Application US/10750185
Sequence 58068, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANY: CATTER, DATRICK

APPLICANY: CATTER, DATRICK

ITTLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

ITTLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 2001.21.471C15

CURRENT APPLICATION NUMBER: US/11/108,172

CURRENT FILING DATE: 2005-04-15

PRIOR APPLICATION NUMBER: US 10/025,380

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-12-19

PRIOR FILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: US 09/922,217

PRIOR APPLICATION NUMBER: US 09/833,263

PRIOR APPLICATION NUMBER: US 09/833,263

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-28

PRIOR APPLICATION NUMBER: US 09/649,811

PRIOR PRIOR APPLICATION NUMBER: US 09/649,811

PRIOR PRIOR APPLICATION NUMBER: US 09/649,811

PRIOR FILING DATE: 2000-08-28

PRIOR PRIOR APPLICATION NUMBER: US 09/649,811

PRIOR PRIOR APPLICATION NUMBER: US 09/649,811
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NUMBER OF SEQ ID NOS: 1130
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 547
LENGTH: 399
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Best Local
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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FILING DATE: 2000-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 09/476,296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 09/480,321 FILING DATE: 2000-01-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 09/519,444 FILING DATE: 2000-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 09/575,251 FILING DATE: 2000-05-19
                                                                                                                                                                                                                                                                                                                                                                                                        115 AAAGTAAAAATGTAATAATTGAAATAGAAAAAGTTTGGTAAATTCAACACCTACGAATGA 56
                                                                                                                                                                                                                                                                                                     55 TAGAACACCAAGAWRTYTATTAGAAGAAAACTTTTGAGACCTGC
                                                                                                                                                                                                                                                                                                                                                     65 TAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                5 AAAGCAGAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Skeiky,
                  KERR, Richard
ROSENFELD, David
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Vedvick Thomas S.
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Smith, Carole L.
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Stolk, John A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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des, Michael J.
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Pred. No. 3.5;
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APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
FILE OF:INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 58068
LENGTH: 1135
TYPE: DNA
ORGANISM
US-10
RESULT 15

US-10-986-501-27/c

; Sequence 27, Application US/10986501

; Publication No. US20050244845A1

; GENERAL INFORMATION:
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LENGTH: 1765
TYPE: DNA
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Best Local S
Matches 49
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Publication No. US20050260603A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: MMII100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HOLM, Tom
APPLICANT: BATES, Scephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MMI GENOMICS, 1
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, Dav
                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIN version 3.1
                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bovine 19866880384477
                                                                                                                                                                                                                                                                      Match 3.2%;
Local Similarity 64.5%;
                                                                                                                                                     539
                                                                                                                      105
                                                                                                                                                                                                                      479 CAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCAATGCAATTTATAGTC 538
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                                                                                                                                                                                                                                                          49;
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                                                                                                                      TGGCCCCCTGCATAAG
                                                                                                                                                     TGTCTTACCCAATGAG
                                                                                                                                                                                   CAAGTAAATATTTTGAAGTTCTCATCTACTTCTTTGCTTTTCTGCATGCCAAGGACAGTG
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                                                                                                                                                                                                                                                        Conservative
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ilarity 64.5%;
Conservative
                                                                                                                                                     55.4
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Pred. No. 6.1;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 1307
TYPE: DNA
ORGANISM: Homo sapiens
US-10-986-501-27
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Search completed: December 5, 2005, 08:05:52 Job time : 323.456 secs
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PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR APPLICATION NUMBER: PC7/US98/16235
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: PC7/US98/16235
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.2%; Score 32.4; DB 6; Length 1307; Best Local Similarity 50.5%; Pred. No. 8.7; Matches 111; Conservative 0; Mismatches 101; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: PEO13P2C1
CURRENT APPLICATION NUMBER: US/10/986,501
CURRENT FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-07-18
PRIOR FILING DATE: 2003-06-9,730
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-10-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/056,364 PRIOR FILING DATE: 1997-08-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                590 ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAAATGG 649
                                                                                                                  401 AGCCCATTTTTCATCTTCTTTGAAGCATCTTTTAAATATT 362
                                                                                                                                                         770 TAGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATT 809
                                                                                                                                                                                                                                 461 ATATTGAACAAGTAAATGGCTCCTTCTCCTGAACAGGGGTTAACCAGTTTTACAAACATT
                                                                                                                                                                                                                                                                                  710 CTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGC 769
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
   1017
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1: /cgn2 6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

3: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

4: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

5: /cgn2 6/ptodata/1/pubpna/US10A PUBCOMB.seq:*

6: /cgn2 6/ptodata/1/pubpna/US10B PUBCOMB.seq:*

6: /cgn2 6/ptodata/1/pubpna/US10B PUBCOMB.seq:*

7: /cgn2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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US-10-696-639-15
US-10-105-044-1
US-10-408-009-1
US-10-856-109-1
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US-10-753-195-1
US-10-753-195-1
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US-10-9895-13-878
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US-10-011-095-1
US-10-010-667A-1
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US-10-294-025-878
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8858.046 Million cell updates/sec
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Sequence 6, Appli	Sequence 6, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 5120, Ap	Sequence 191, App	Sequence 19910, A	Sequence 16445, A	Sequence 396, App	Sequence 428, App	Sequence 1, Appli	Sequence 7046, Ap	Sequence 1811, Ap	Sequence 42, Appl	Sequence 16, Appl	Sequence 1, Appli	Sequence 42, Appl	Sequence 16, Appl	Sequence 1130, Ap	Sequence 713, App

ALIGNMENTS

RESULT 1 US-10-696-639-15

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CURRENT APPLICATION NUMBER: US/10/696,639
CURRENT FILING DATE: 2003-10-29
PRIOR APPLICATION UMBER: 60/422,176
PRIOR FILING DATE: 2002-10-29
NUMBER OF SEQ ID NOS: 3114
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 1177
TYPE: DNA
ORGANISM: homo sapiens
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Publication No. US20050037439A1

GENERAL INFORMATION:
APPLICANT: Pharmacia Corporation
APPLICANT: Bourner, Maureen J.

TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
FILE REFERENCE: 0.1040/1
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Best Local Similarity
Matches 1017; Conserv
306
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Sequence 1, Application US/10165044

Publication No. US20030149531A1

GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Rene S. Hubert
APPLICANT: Douglas Saffran

APPLICANT: Daniel E.H. Afar
APPLICANT: Steven Chappell Mitchell
APPLICANT: Mary Faris
APPLICANT: Mary Faris
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO;
FILE REFERENCE: 51158-20016.02

CURRENT APPLICATION NUMBER: US 60/087,520
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR PILING DATE: 1998-06-01

PRIOR APPLICATION NUMBER: US 09/323,873

PRIOR FILING DATE: 1998-06-01

PRIOR APPLICATION NUMBER: US 09/323,873

PRIOR FILING DATE: 1998-06-01
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; TYPE: DNA
; ORGANIEM: Homo sapi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1
US-10-165-044-1
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Similarity 100.0%; Pred. No. 7e-277;
17; Conservative 0; Mismatches 0
                                   GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT
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US-10-408-009-1
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Publication No. US20040072196A1
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
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Best Local Similarity 100.0%;
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NAME/KEY: CDS
LOCATION: (64)...(1083)
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ORGANISM: Homo
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Pred. No. 7e-277;
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                                      APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
ITITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO
FILE REFERENCE: 511582001607
FULE REFERENCE: 511582001607
CURRENT APPLICATION NUMBER: US/10/857,785
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR APPLICATION NUMBER: US 60/087,520
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR FILING DATE: 1998-06-30
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US-10-857-785-1
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 SEQ ID
 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 1
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Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0
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                                     AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTTCCAATTGTT
                                                                              GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT
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GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT
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Sequence 1, Application US/10856109
Publication No. US20040219591A1
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Daniel E. Afar
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SEPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO;
FILE REFERENCE: 511582001606
CURRENT APPLICATION NUMBER: US/10/856,109
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1999-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-30
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Best Local S
Matches 1017
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SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 1
LENGTH: 1193
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LOCATION: (64)...(1083)
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US-10-830-899-2

Sequence 2, Application US/10830899

Publication No. US20040253232A1

GENERAL INFORMATION:

APPLICANT: Jakobovits, Aya

APPLICANT: Etessami, Soudabeh

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Herez-Villar, Jouan

APPLICANT: Perez-Villar, Jouan

APPLICANT: Faris, Mary

APPLICANT: Raitano, Arthur B.

TITLE OF INVENTION: Antibodies and Molecules Der.

TITLE OF INVENTION: Antibodies and Molecules Der.

TITLE OF INVENTION NUMBER: 09/323,873

PRIOR APPLICATION NUMBER: 09/323,873

PRIOR APPLICATION NUMBER: 10/010,667

PRIOR APPLICATION NUMBER: 10/010,667

PRIOR APPLICATION NUMBER: 10/010,95

PRIOR APPLICATION NUMBER: 10/236,878

PRIOR FILING DATE: 2001-12-06

PRIOR APPLICATION NUMBER: 10/236,878

PRIOR APPLICATION NUMBER: 10/236,878

PRIOR FILING DATE: 2001-09-06

PRIOR APPLICATION NUMBER: 09/455,486

PRIOR APPLICATION NUMBER: 09/455,486

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1999-10-06
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; SOFTWARE: FASTSEQ for Windows Ve; SEQ ID NO, 2
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)...(1085)
US-10-830-899-2
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        TCTCTGGGAATTGTGGGAATTGGCAATACTGGCTCTGTTTGGCTGTGACATCTATTCCATCT
                                                                                                                                               TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCCTGTGACATCTATTCCATCT
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; LOCATION: (64)...(1191)
US-10-753-195-1
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CURRENT APPLICATION NUMBER: US/10/753,195
CURRENT FILING DATE: 2004-01-06
PRIOR APPLICATION NUMBER: US/10/165,044
PRIOR FILING DATE: 2002-06-06
PRIOR PPLICATION NUMBER: US 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 09/455,486
PRIOR APPLICATION NUMBER: WO 99/62941
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: WO 99/62941
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: WO 99/62941
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PRIOR APPLICATION NUMBER: WO 99/62941
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PRIOR FILING DATE: 1990-06-01
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 1017; Conserv
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SEQ ID NO 1
LENGTH: 1193
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APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raita
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo e
FEATURE:
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                          CTTCAGCACACAGAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
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Daniel E.H. Afar
Steven Chappell Mitchell
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for Windows Version
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100.0%; Pred. No. 7e-277;
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APPLICANT: Daniel E. Afar
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Arbur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO
FILE REFERENCE: 51158201612
FULL REFERENCE: 51158201612
FURRENT APPLICATION NUMBER: US/10/752,421
CURRENT APPLICATION NUMBER: US/8/45,486
PRIOR APPLICATION NUMBER: US/9/455,486
PRIOR APPLICATION NUMBER: US/9/453,486
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; LOCATION: (64)...
US-10-752-421-1
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PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: US 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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Best Local Similarity 100.
Matches 1017; Conservative
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ORGANISM: Homo |
FEATURE:
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SOFTWARE: PASTSEQ for Win
SEQ ID NO 2
LENGTH: 1193
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (66)...(1085)
US-10-861-662-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Etessami, Soudabeh
APPLICANT: Etessami, Soudabeh
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Grerz-Villar, Juan
APPLICANT: Meyrick Morrison, Karen Jane
APPLICANT: Faris, Mary
APPLICANT: Gudas, Jean
APPLICANT: Gudas, Jean
APPLICANT: Raitano, Arthur B.
TITLE OF INVENTION: Antibodies and Molecules Derived
TITLE OF INVENTION: therefrom that Bind to STEAP-1 Proteins
TITLE OF INVENTION: therefrom that Bind to STEAP-1 Proteins
TITLE OF INVENTION: therefrom that Bind to STEAP-1 Proteins
TITLE OF INVENTION: therefrom that Bind to STEAP-1 Proteins
TITLE OF INVENTION: 1518-20016.26
CURRENT APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 2004-06-04
PRIOR APPLICATION NUMBER: 10/010,667
PRIOR APPLICATION NUMBER: 10/010,667
PRIOR APPLICATION NUMBER: 10/011,095
PRIOR APPLICATION NUMBER: 10/011,095
PRIOR APPLICATION NUMBER: 10/011,095
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR APPLICATION NUMBER: 09/455,486
PRIOR APPLICATION NUMBER: 09/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEO ID NOS: 103
COFTMANDER: 540/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEO ID NOS: 103
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US-10-861-662-2
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Best Local Similarity 100.0%;
Matches 1017; Conservative (
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CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA
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Pred. No. 7e-277;
0; Mismatches 0;
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RESULT 10
US-09-759-143-878
US-09-759-143-878
Sequence 878, Appl
Patent NO. US2007
GENERAL INFORMATI
APPLICANT: Mitc
APPLICANT: Mitc
APPLICANT: Harx
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APPLICANT: Kale
APPLICANT: Reti
APPLICANT: Reti
APPLICANT: Sto
Sequence 878, Application US/09759143
Patent NO. US20022248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Rate, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Boy, Craig H.
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APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Neekky, Yeair A.W.
APPLICANT: Neekky, William
TITLE OF INVENTION: COMPOSITIONS AND METHOD
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE C
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-759-143-878
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; ORGANISM: Homo sapiens
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SOFTWARE: FastSEQ for
SEQ ID NO 878
LENGTH: 1195
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Patent No. US2002005.977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
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APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
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Retter, Marc W.
Stolk, John A.
Day, Craig H.
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Dillon, Davin C.
Mitcham, Jennifer I
Harlocker, Susan L.
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Skeiky, Yasir A.W.
Hepler, William
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Carter, Darrick
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       ; Sequence 878, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
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APPLICANT: FARGET, GATY R.
APPLICANT: FARGET, GATY R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CUBRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASUSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
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APPLICANT: Micc
APPLICANT: Har
APPLICANT: Yian
APPLICANT: Kalı
APPLICANT: Reti
APPLICANT: Sto
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Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A
                                                TCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
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Mitcham, Jennifer L.
Harlocker, Susan L.
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Kalos, Michael D.
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Vedvick, Thomas S
Carter, Darrick
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Sequence 878, Application US/0985814

Publication No. US20020193296A1

GENERAL INFORMATION:

APPLICANT: XJ. Jiangchun

APPLICANT: Dillon, Davin C.

APPLICANT: Micham, Jennifer L.

APPLICANT: Hicham, Jennifer L.

APPLICANT: Jiang, Yuqiu

APPLICANT: Jiang, Yuqiu

APPLICANT: Stolk, John A.

APPLICANT: Stolk, John A.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Li, Samuel X.

APPLICANT: Li, Samuel X.

APPLICANT: Hepler, William T.

APPLICANT: Hepler, William T.

APPLICANT: Henderson, Robert A.

APPLICANT: Hural, John

APPLICANT: Hural, John

APPLICANT: Hural, John

APPLICANT: Houghton, Raymond L.

APPLICANT: Houghton, Raymond L.

APPLICANT: Foy, Teresa

APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE:; PastSEQ for Windows Version
SEQ ID NO 878
LENGTH: 1195
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Weagher, Madeleine Joy
APPLICANT: Weagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT FILING DATE: 2001-12-10
UNMBER OF SEQ ID NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
SOFTWARE: FASTESQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-878
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US-10-012-896-878
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APPLICANT: Dillon, Davin C.
APPLICANT: Miccham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: Retter, Marc W.
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Stolk, John A.
Stolk, John A.
Day, Craig H.
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                                                      CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
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Kalos, Michael D.
Retter, Marc W.
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
Henderson, Robert A.
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Li, Samuel X.
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Search completed: December Job time : 952.415 secs 5, 2005, 07:54:11

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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ALIGNMENTS

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; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1083)
US-09-455-486-1
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APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saifran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANT
TITLE OF INVENTION: NOVELSE BEPENTINE TRANSMEMBRANE ANT
TITLE OF INVENTION: NOVELSE BEPENTINE TRANSMEMBRANE ANT
TITLE OF INVENTION: NOVELSE BEPENTINE TRANSMEMBRANE ANT
TITLE OF INVENTION NUMBER: 109/9455,486
CURRENT APPLICATION NUMBER: 109/323,873
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
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US-09-455-486-1
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SOFTWARE: FastSEQ for
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 1017; DB 3; Best Local Similarity 100.0%; Pred. No. 2.5e-304; Matches 1017; Conservative 0; Mismatches 0;
                    181
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FastSEQ for Windows Version
CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
                                                                        CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA
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RESULT 2
US-09-323-873A-1
; Sequence 1, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Marthur B. Raitano
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: NOVEL SERPENTINE
TOTAL REPERBENCE: 129-165-01
FILE REFERENCE: 129-165-01
FRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/091,183
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                      TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
ITITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
US-09-685-166A-878
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US-09-685-166A-878
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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Best Local
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APPLICANT:
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Kalos, Michael D
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas (Carter, Darrick
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US-09-679-426-878
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              APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHOL
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE (
TITLE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
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APPLICANT:
APPLICANT:
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APPLICANT:
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   SOFTWARE:
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Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Mitcham, Jennifer L.
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; TYPE: DNA
; ORGANISM: Homo sapiens
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                                  GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT
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APPLICANT: W. Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William
ITILE OF INVENTION: COMPOSITIONS AND METHOD:
ITILE OF INVENTION: COMPOSITONS AND METHOD:
ITILE OF INVENTION: DIAGNOSIS OF PROSTATE C:
FILE REFERENCE: 210121.427C23
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 878
LENGTH: 1195
TYPE: DNA
ORGANISM: Homo sapiens
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                 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA
                                                                                    TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
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                                                                  TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
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APPLICANT: Hubert, Rene S.

APPLICANT: Hubert, Rene S.

APPLICANT: Leong, Kahan

APPLICANT: Saffran, Arthur B.

APPLICANT: Saffran, Douglas C.

APPLICANT: Mitchell, Steve Chappell

APPLICANT: Mitchell, Steve Chappell

TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF

FILE REFERENCE: $11582001601

CURRENT APPLICATION NUMBER: US/10/010,667A

CURRENT APPLICATION NUMBER: 09/323,873

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1998-06-01

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR FILING DATE: 1998-06-30

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1195

TYPE: DNA

ORGANISM: Homo Sapiens
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GENERAL INFORMATION:
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APPLICANT: Millon, Davin
APPLICANT: Mitcham, Jenn:
APPLICANT: Harlocker, Su
APPLICANT: Jiang, Yuqiu
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Patent No. 6943236
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 1017; Conservative
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APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
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Li, Samuel X.
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Vedvick, Thomas S
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Mitcham, Jennifer L.
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Meagher, Madeleine Joy
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Pred. No. 2.5e-304;
Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2686
LENGTH: 1147
TYPE: DNA
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PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                             Query Match
Best Local Similarity
Matches 1016; Conserv
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                  ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
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 ATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA
                                                                Conservative
                                                                               99.8%;
99.9%;
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                                                                Score 1015.4; DB 3;
Pred. No. 7.8e-304;
0; Mismatches 1;
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RESULT 9
US-09-323-873A-6
US-09-323-873A-6
; Sequence 6, Application US/09
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
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APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: WOVEL SEREBNTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
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; SEQ ID NO 6
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-323-873A-6
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99.5%;
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Pred. No. 1.2e-224;
0; Mismatches 4;
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APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Stephen C. Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.17-US-11
CURRENT APPLICATION NUMBER: US/09/455,486
CURRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 34
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; ORGANISM: Homo sapiens
US-09-455-486-4
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SEQ ID NO 4
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Best Local Similarity
Matches 763; Conserv
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TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
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PATENT PILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICANT: MICCATION SERIES THEREOF
FILE REFERENCE: 511582001601
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-03
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
LEBROTH: 3627
TYPE: DNA
ORGANISM: Homo sapiens
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Local Similarity 99.5%;
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GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA
                                                TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
                                                                                                                                                                                  CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
                                                                                                                  <u>.</u>.
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Pred. No. 1.2e-224;
0; Mismatches 4;
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; ORGANISM: Homo sapien
US-09-439-313-342
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US-09-439-313-342/c
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Lou
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CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOPTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 592
                                                                                                                                                                          Query Match
Best Local Similarity
Matches 516; Conserv
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Patent No. 6329505
GENERAL INFORMATION:
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APPLICANT:
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APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
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                                                 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
                                                                           AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA
                                                                                                                           ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA
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   CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
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Reed, Steven G.
Kalos, Michael
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Retter, Mark
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                                                                                                                                                                         Score 516; DB 3; Length 592; Pred. No. 2.4e-149; 1; Mismatches 1; Indels
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TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAACAAGTCTTGCCAATG
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RESULT 13
US-09-352-616A-342/c
; Sequence 342, Application US/09352616A
; Patent No. 6395278
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SEQ ID NO 342
LENGTH: 592
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Jiang, Yuqui
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR U
FILE REFERENCE: 21011.4.7208
CURRENT APPLICATION UNMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTMARER: FESTER FOR MINING WARRENDERS OF SEQ ID NOS: 472
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Best Local Similarity 99.6%;
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                         ATAGCATCTCTGACTTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
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ATAGCATCTCTGACTTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT
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Pred. No. 2.4e-149;
1; Mismatches 1;
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APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THEA

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.42717C17

CURRENT APPLICATION NUMBER: US/09/636,215

CURRENT FILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 852

SOFTWARE: FastSEQ for Window

TYPE: DNO

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Best Local Similarity
Matches 516; Conserv
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Retter, Marc W.
Stolk, John A.
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             ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT
                                                            CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
                                                                                                                                              AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA
                                                                                                                       CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA
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Dillon, Davin C.
Mitcham, Jennifer L.
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Kalos, Michael D.
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Pred. No. 2.4e-149;
1; Mismatches 1;
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 342
LENGTH: 592
TYPE: PARK
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APPLICANT: Xilangchun, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
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Best Local S
Matches 516
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milarity 99.6%;
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Search completed: December 5, 2005, 03:19:40 Job time : 205.756 secs

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Copyright

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

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SUMMARIES

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1017	1017	1017	1017	1017	1017	1017	1017	1017	1017	1017	1017	1017	1017	1017	1017	1017	1017	1017	Score	
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Adp88258 Prostate	Adn39395 Cancer/an	Adn39812 Cancer/an	Adg26744 Human pro	Aad62763 Human STE	Aad63162 Human STE	Adb14328 Human pro	Adb75572 Prostate	Acc95695 Prostate	Abk92128 Prostate		Aca59968 Prostate	Aas64160 Human pro	Aah93924 P789P ful	Ady92698 Human STE	Acd02597 cDNA enco	Aad07067 Human six	Aaz49395 Human STR	Adv73174 Human col	Description	

The invention relates to an antibody immunospecifically binds to p-cadherin or its fragment. The antibody is useful in preparing a composition for treating or preventing a cancer-associated disorder. present sequence represents a gene upregulated in human colon cancer cells.

The

Disclosure; SEQ ID NO 15; 257pp; English.

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ALIGNMENTS

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New antibody that immunospecifically binds to p-cadherin, useful in preparing a composition for treating or preventing a cancer-associated disorder.
                                                                                                                  Bourner MJ, Bu
Mazzarella RA,
                                                                                             WPI; 2005-039958/04.
P-PSDB; ADV73212.
                                                                                                                                                                      28-OCT-2003; 2003WO-US034019
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Pred. No. 2.6e-276;
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AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG

1082

CC This sequence represents cDNA encoding a novel human protein, STRAP-1 CC (serpentine transmembrane antigen of the prostate). STRAP-1 is the CC prototype member of the STRAP family of proteins (AAY58194-Y58197) which CC exhibit a high degree of structural conservation, but which show no CC significant structural homology to known human proteins. The STRAP-1 gene CC lila membrane protein and is expressed predominantly in prostate cells in CC cormal human tissues. Structurally, STRAP-1 is a 339 amino acid protein CC caracterised by six transmembrane domains and intracellular N- and C-CC termini, suggesting that it folds in a "serpentine" manner into three CC extracellular and two intracellular loops. STRAP-1 mRNA and protein CC expression is maintained at high levels and throughout all stages of CC prostate cancer. STRAP-1 mRNA and/or protein is also overexpressed in CC certain other cancers, including bladder, colon, pancreatic and ovarian cancer. The function of the STRAP proteins is not known. They may be ion CC channels (from the presence of six transmembrane domains, a feature which is shared by certain ion channels) or gap-junction proteins (from the context transmembrane domains, a feature which can shared by certain in staining). STRAP-1 and STRAP-2 are cell-surface context.

Claim

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Fig 1A; 83pp;

English

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RESULT 2
AAZ49395
ID AAZ4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   particularly for prostatic
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30-JUN-1998;
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(HUBE/)
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DB; AAY58194.
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antigen of the prostate)"
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Hickory Charles Containing

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Matches 1017
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                                                                                                                                                                                                              CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATTGGAGATTTATGTG
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Faris M,
         The present sequence is human six transmembrane epithelial antigen of the prostate (STEAP)-1 clone 10 CDNA. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP is a member of cell surface 7922.3 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting growth or killing cells expressing STEAP in a patient, comprises administering a vaccine
                                                                                                                                       New STEAP proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytostatic; antiprollferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-1; STEAP-1; chromosome 7p22.3; cancer; prostate; colon; bladder; lung; ovarian; pancreatic; ss.
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                                                                                                      Example
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                                                                                                                                                                            WPI; 2001-367804/38
P-PSDB; AAE02780.
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Jakobovits
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                                                                                                      1A-1B; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                              the prostate (STEAR)-1"

/note= "CDS does not include stop codon"
/transl except= (pos:1078. .1086, aa:Leu-Asn)
/note= "Inframe stop codon alters the reading
/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 64. .1191
                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "Human six transmembrane
patient.
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                                                                                                                      Query Match
Best Local Similarity
Matches 1017; Conserv
                                                                                                                                                                                                                                                                                        The invention describes a composition comprising a substance that modulates the status of a protein (I) of 340 or 283 amino acids, or of any of the 15 sequences of 259 amino acids, given in the specification, or a molecule that is modulated by the protein, where the status of the cell that expresses the protein is modulated. The compositions, proteins, polynucleotides and methods are useful for treating and detecting cancer. The STEAP-1-related proteins are useful for generating cancer vaccines. The polynucleotides are useful as tools for delineating, with greater precision, cytogenetic abnormalities in the chromosomal region that encodes STEAP-1 that may contribute to the malignant phenotype. This sequence encodes a variant of human six transmembrane epithelial antigen of the prostate or STEAP-1
                                                                                                                                                                                                                                         Sequence 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising a substance that modulates the status of STEAP-1-related protein, useful for treating and detecting cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2001; 2001US-0317840P.
05-APR-2002; 2002US-0370387P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEAP-1; six transmembrane epithelial antigen of the prostate; cancer; cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-2003 (first entry)
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Best Local Similarity
Matches 1017; Conserv
                                                                                                                                                                       The invention relates to cell surface serpentine transmembrane antigens predominantly expressed in the prostate termed as six transmembrane epithelial antigen of prostate (STEAP-2) and their corresponding nucleic acid sequences. STEAP-2 DNA is useful for diagnosing or treating prostate cancer. It can be used as a primer or probe for the amplification and/or detection of STEAP genes and as a tool for modulating or inhibiting the expression of the STEAP genes. STEAP-2 DNA is also useful in cancer vaccines for the generation of therapeutic or prophylactic immunity against prostate cancer. STEAP antibodies are useful in antibody therapy. The present sequence is the human STEAP-1 cDNA. Human STEAP-1 gene maps within chromosome 7p22 (7p2.3).
                                                                                                                                                    Sequence
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(HUBE/)
(RAIT/)
                                                                                                                                                                                                                                                                                                                                Example 1;
                                                                                                                                                                                                                                                                                                                                                                   Novel isolated polynucleotide that encodes six transmembrane epithelial antigen of prostate polypeptide, useful for diagnosing or treating
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06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine; antibody therapy; immune stimulation; gene amplification; prostate tumor; cytostatic; andrology; genitourinary disease; neopla cancer; six transmembrane epithelial antigen of prostate 1; STEAP-1;
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) HUBERT R S.
) RAITANO A B.
) SAFFRAN D.
) MITCHELL S C.
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                AATTTAGAAGAAGAAGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA
                                                  ATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA
                                                                  ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA
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ilarity 100.0%;
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Best Local Similarity
Matches 1017; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAMO1115 to AAMO1318 represent polynucleotide and amino acid sequences used in the exemplification of the prosent invaries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xu J, Dillon DC, Mit Kalos MD, Fanger GR, Wang A, Meagher MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide encoding a prostate-specific protein, monitoring and treating prostate cancer in a patient and
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CORP
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The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xu J, Dillon
Fanger:GR, R
Li SX, Wang
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P-PSDB; AAU69927.
                                                                                                                                                                                                                                                                                                                Claim 1; Page 548; 579pp;
                                                                                                                                                                                                                                                                                                                                                          human prostate-specific diagnosis and treatment
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                                                                                                                                                                                                                                                                                                                  English
                                                                                                                                                                                                                                                                                                                                                            polypeptides and polynucleotides useful of cancer, especially prostate cancer.
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Query Match Best Local Similarity Matches 1017; Conserv μ Conservative 100.0%; 0. Score 1017; DB 4; Pred. No. 2.6e-276; Mismatches 0 Indels Length 0 Gaps 60 0

Sequence 1195 BP; 382 A;

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer therapy associated cDNA. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MCNE/)
(HOUG/)
(DBAS/)
(FOYT/)
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DB; ABU71821.
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Y DE BASSOLS
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GTTTCCATCACTCTTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA
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Pred. No. 2.6e-276;
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25-FEB-1997

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13-JUI-1999

13-JUI-1999

12-NOV-1999

14-NAN-2000

27-MAR-2000

27-MAR-2000

12-MAY-2000

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Matches 1017; Conserv
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Fanger G
Li SX,
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                                                                                                                                                                                                                                                                                                                                                         New prostate-specific polynucleotides for diseases, in particular prostate cancer, progression of cancer.
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06-SEP-2000;
02-OCT-2000;
10-OCT-2000;
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LI S X.
WANG A.
SKEIKY Y A W
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MITCHAM J L.
HARLOCKER S I
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KALOS M D .
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
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TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
                                                                            ATAGCATCTCTGACTTTTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCACT
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gene therapy; gene; ds.
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2001US-0276889F.
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Gish
                                                                                                                                                            Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
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from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer-associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABK92115-ABK92263 represent prostate cancer-associated polynucleotide The present invention relates to methods of detecting a prostate cancerassociated transcript in a cell from a patient. The method comprises
contacting a biological sample from the patient with prostate cancerassociated polynucleotides (designated PC genes) that selectively
hybridise to a sequence that is at least 80% identical to them. The
prostate cancer-associated polynucleotide sequences are differentially
expressed in prostate tumour tissue or in prostate cancer and are derived sequences

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Kalos MD, I
Carter D, I
Mcneill PD,
Deng T;
New prostate-specific proteins and genes, useful in gene therapy, particularly for stimulating an immune response in a patient, or prostate cancer in a patient, as well as for diagnosing prostate in a patient.
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29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
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MD, Fanger GR, Rette
r D, Li SX, Wang A,
Il PD, Houghton RL, V
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KGR, Retter MW, Stolk JA, Day CH, Vedvick
Wang A, Skeiky YAW, Hepler WT, Hural J;
ton RL, Vinals Y De BassolsC, Foy TM, Wata
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                                                                                                  The invention relates to newly discovered cancer markers associated with CC the cancerous state of prostate cells. Also disclosed is a method of CC assessing whether a patient is afflicted with prostate cancer. The method CC of the invention involves assessing whether a patient is afflicted with CC prostate cancer by comparing the level of expression of a marker in a CC patient sample and the normal level of expression of the marker in a CC control non-prostate cancer sample, where a significant increase in the CC level of expression of the marker in the patient sample and the normal CC nucleic acids of the invention are useful for diagnosing or treating CC prostate cancer, and may be useful in gene therapy. Sequences given in CC ADB7517-ADB75631 represent marker cDNA and proteins. Note: The sequence CC data for this patent did not form part of the printed specification, but CC was obtained in electronic format directly from WIPO at CC tp. wipo.int/pub/published_pct_sequences.
                        Query Match
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22-AUG-2001; 2001US-0314356P.
25-SEP-2001; 2001US-0325020P.
12-DEC-2001; 2001US-0341746P.
05-MAR-2002; 2002US-0362158P.
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660 599 600 605 540 545

785 720 725 420

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365 300 305 240

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Human prostate specific full length cDNA P789P

immunostimulant

18-DEC-2003 (first entry)

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18-NOV-1999
14-JAN-2000;
27-MAR-2000;
09-MAY-2000;
11-MAY-2000;
11-MAY-2000;
12-MAY-2000;
27-JUN-2000;
29-AUG-2000;
29-AUG-2000;
29-AUG-2000;
06-SEP-2000;
06-OCT-2000;
07-OCT-2000;
07-OCT-2000;
08-OCT-2000;
09-NOV-2001;
10-DEC-2001;
The invention relates to an isolated polypeptide comprising no more than 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The peptides comprise a fragment ADB13563 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles. ADB13563 is a polypeptide encoded by a human prostate specific cDNA, one of 648 disclosed as new. Also included are nucleic acids encoding the proteins and peptides, expression vectors, a host cell transformed with the vector, an isolated antibody (or antigen binding fragment) that specifically binds to the protein or peptide, detecting the presence of a cancer in a patient (comprising contacting a patient sample with a binding agent that binds to the peptides or a polypeptide appearing as ADB13558, detecting the amount of polypeptide that binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUL-1998;
23-SEP-1998;
15-JAN-1999;
09-APR-1999;
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                                                                                                                                                                                                      New isolated polypeptide for use in a vaccine for stimulating an iresponse, or for treating or diagnosis cancer, preferably prostate
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2000US-00436857
2000US-005368100
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CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC coff value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC cancer in a patient and treating prostate cancer in a patient comprising
CC from a patient with the peptides or antigen presenting cells that express
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC prosence of cancer in a patient. The peptides, nucleic acids encoding, or
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC prostate cancer in a patient. The present sequence is a known cDNA
CC showing sequence similarity to one of the disclosed human prostate
CC specific cDNAs. Note: Except where otherwise indicated, the sequence data
CC obtained in electronic format directly from USPTO at
CC sequata.uspto.gov/sequence.html?DocID=20030185830.
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Query Match Best Local 9 Sequence 1195 BP; 382 A; 100.0%; Score 1017; 100.0%; Pred. No. 2.6 tive 0; Mismatches 221 C; 233 G; 359 T; 0 U; 0 Other; DB 10; Length 1195

Matches 1017;

Similarity

Conservative

Ş В S 밁 δ 문 δ 밁 Ş 밁 Ş 밁 S δ 밁 Ś 밁 밁 S 601 481 486 421 426 306 361 366 301 246 181 186 121 126 9 Ь CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCCAGCATGCTAAAAAGA TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA **AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA** ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAAATGAAGCCTAGGAGA ATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 0 Indels 0, Gaps 600 605 545 480 660 665 540 485 420 425 360 300 180 185 120 125 60 365 305 240 0

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RESULT 14

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                                          The present invention relates to a method of prognosticating metastasis in a breast cancer patient involves identifying differential modulation of each gene relative to the expression of the same genes in a normal population in combination of genes. The invention is useful for prognosticating breast cancer in a patient. The present sequence is human STEAP (six transmembrane epithelial antigen of the prostate) DNA used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                              Prognosticating metastasis in a breast cancer patient comprises identifying differential modulation of each gene relative to the expression of the same genes in a normal population in combination
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                                                  GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT
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Best Local Similarity
Matches 1017; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for diagnosing cancer. The method comprising identifying differential modulation of each gene (relative to the expression of the same genes in a normal population) in a combination of genes. The method, diagnostic portfolio and the kit are useful in diagnosing cancer. The method may also be used for determining gene expression profiles. The present sequence is human STEAP (six transmembrane epithelial antigen of the prostate) DNA used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing cancer comprises identifying differential modulation of gene (relative to the expression of the same genes in a normal population) in a combination of genes.
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Search completed: December 4, 2005, 21:08:44
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AR371039 Sequence	AR367143 Sequence	AR278447 Sequence	BD242240 Compounds	AC162380 Pan trogl	AC161278 Pan trogl	AC104475 Pan trogl	AC142337 Pan trogl	AC147308 Pan trogl	AC004969 Homo sapi	AC021898 Homo sapi	BC066301 Homo sapi	AY029584 Mus muscu	BD192004 Modulator	CQ777614 Sequence	AF297098 Mus muscu	BC061023 Mus muscu	AX155248 Sequence		AR617056 Sequence	AR366784 Sequence	BD232188 Novel ser	_	CS045211 Sequence		_	CS031875 Sequence

ALIGNMENTS

RESULT 1 BD232184 LOCUS DEFINITION VERSION KEYWORDS FEATURES COMMENT REFERENCE SOURCE ACCESSION JOURNAL TITLE AUTHORS ORGANISM source Novel scrpiginous transmembrane antigen expressed in and utilization thereof.

BD332184

BD332184.1 GI:33041954

JP 2002517184-b/1 PF 01-JUN-1999 JP 2000552151
PR 01-JUN-1998 US 60/091183 PI 01-JUN-1998 US 60/091183 PI DANIEL B APAR, REME S HUBERT, KAHAN LEONG, ARTHUR B RAITANO PI DOUGLAS C SAFFRAN, PN PD PF Novel serpiginous transmembrane antigen expressed in human cancer and utilization thereof 1 (bases 1 to 1193)
Afar,D.E., Hubert,R.S., Leong,K., Raitano,A.B., Saffran,D.C. and Mitchell,S.C. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. Patent: JP 2002517184-A 1 18-JUN-2002; UROGENESYS INC Homo sapiens Homo sapiens (human) Homo sapiens (human) JP 2002517184-A/1 18-JUN-2002 Novel serpiginous transmembrane antigen expressed in human cancer and STEPHEN CHAPPELL MITCHELL C12N15/09, A61K38/00, A61K38/00, A61K38/00, A61K39/395, A61P35/00, C07K14/47, C07K16/18, utilization thereof C12P21/00, C12P21/08, C12Q1/68, G01N33/574, C12N15/00, A61K37/02, C12N5/10, /organism='Homo sapiens (human)'.
Location/Qualifiers organism="Homo sapiens"/ Location/Qualifiers PAT 17-JUL-2003 1 human cancer გ

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Patent: US 6833438-A 1 21-DEC-2004;
Agensys, Inc.; Santa Monica, CA
Location/Qualifiers
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Afar, D.E., Hubert, R.S., Raitano, A.B.,
Mitchell, S.C.
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CQ776742 1195 bp DNA linear PAT 11-MAR-2004 Sequence 428 from Patent EP1394274. CQ776742 CQ776742.1 GI:45380132 Homo sapiens (human)	781 TCCCTTCTACTGGCACATACACGCATTGATTTTTGCCTGGAATAAGTGGTGATAATAAGTGGTGATAATAAGTGGATAATA	TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT	484 CITICATAATGGAACCAAGTATAAGAAGTTTCCACATTGGATAAGTGGATAAAGTAACA 543 481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTGCTGTACTGCAGTTCATAAGTCTG 540 481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTTTTTTT	TCCCATCAACAATATTTTATAAAATTCCAATCCTGCTCATCAACAAAGTCTTGCCAATG	9

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Agensys, Inc.; Santa
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Afar,D.E., Hubert,R.S.,
Mitchell,S.C.
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/mol_type="genomic |
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of p.
                                                                                                          cancer
Patent: US 6630305-A 878 07-OCT-2003;
Corixa Corporation; Seattle, WA;
WOX;
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ATGGAAAGCAGAAAAGACATCACAAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA
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/mol_type="genomic
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                           Score 1017; DB 6;
Pred. No. 2.6e-231;
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Kalos,M.D., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of p.
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT
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/mol_type="genomic"
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Pred. No. 2.6e-231;
; Mismatches 0;
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
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Unclassified.
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/mol_type="genomic"
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Query Match 100.0%; Score 1017; DB 6; Length 1195; Best Local Similarity 100.0%; Pred. No. 2.6e-231; Best Local Similarity 100.0%; Pred. No. 2.6e-231; Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Indels 0; Gaps 0; ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTTGGAAAATGAAGCCTAGGAGA 60	Unknown. M Unknown. 1 (bases 1 to 1195) 1 (bases 1 to 1195) Afar,D.E., Hubert,R.S., Leong,K., Raitano,A.B., Saffran,D.C. and Mitchell,S.C. Peptides derived from STEAP1 Patent: US 6887975-A 1 03-MAY-2005; Agensys, Inc., Santa Monica, CA Location/Qualifiers 11195 Ce /organism="unknown" /mol_type="genomic DNA"		841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	26 T G G G G G G G G G G G G G G G G G G	
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RESULT 10 AX201105 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	 B & B & B & B	\$ \$ \$ \$	D	8 8 8 8 8	
AX201105 N Sequence 735 from Patent WO0151633. AX201105 AX201105.1 GI:15390890	846 TCCCTTCTACTGGCACAATACACGCATTGATTTTGCCTGGAATAAGTGATATAA 905 841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	TCTCTGGGAATTGTGGGATTGGCAATACTGGCTGTTGGCTGTGACATCTATTCCATCT	546 AGAAAGCAAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCAATTTATAGTCTG 605 541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600 601 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665 601 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665 601 CTACACAAATAAAGAAGATGCCTGGATTGGATGATGTTTGGAGAATGGAAGTTATTATGTG 660 1	361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420	AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA

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Patent: WO 0151633-A 735 19-JUL-2001;
CORIXA CORPORATION (US)
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                                                 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTTAGCAACT
                                                                                              CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
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Query M	ORIGIN	JOURNAL FEATURES	REFERENCE AUTHORS TITLE	SOURCE	DEFINITION ACCESSION VERSION KEYWORDS	RESULT 12 AX926483 LOCUS	g Q	B &	B 9	dg Qy	Qy Db	B 9	D Qy	Qу	gy Db	Db Qy	D Q	Db
Match 100.0%; Score 1017; DB 6; Length 1195;	/or /mo /db	Patent: EP 1355150-A 35 22-OCT-2003; Ortho-Clinical Diagnostics, Inc. (US) Location/Qualifiers	Hominidae; Homo. 1 Wang, Y. Panel of nucleic acid sequences for cancer diagnosis		V Sequence 35 from Patent BP1355150. AX926483 AX926483.1 GI:40246089	AX926483	961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017 	901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960 	841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC	781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATA	721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780 	661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720	601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660 	541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600	481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCA	421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGG	361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420	
RESULT 1	B &	B 8	Db Qy	gb Qy	D Qy	g Q	dg V	Qy Db	Qу	Db Qy	g &	B &	D Qy	g Q	D Q	D 29	в Q	Best Loc Matches
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Mammalia; Eutheria;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Method of selecting a portfolio
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2 (bases 1 to 1195)
Hubert, R.S., Vivanco, I., Chen, E., Rastegar, S., Mitchell, S.C., Madraswala, R., Zhou, Y., Kuo, J., Jakobovits, A., Saffran, D.C. and Afar, D.E.H.
                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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rkofgilsfffavlhaiyslsypmrrsyrykllnmayqqvonkedawiehdwrmei
yvslgivglailallavtsipsvsdsltwrefhyigsklgivslllgtihalifawnk
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ALIGNMENTS

JOURNAL PUBMED REFERENCE AUTHORS REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AY403218 LOCUS DEFINITION ORIGIN FEATURES COMMENT Query Match Best Local Sim Matches 1016; TITLE JOURNAL TITLE gene 2 (bases 1 to 1050) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Submitted (16-NOV-2003) Celera Genomics, 45 Rockville, MD 20850, USA This sequence was made by sequencing genomic them based on alignment. 1. (bases 1 to 1050) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Inferring nonneutral evolution from human-chimp-mouse orthologous Homo sapiens STEAP gene, genomic survey sequence. AY403218 gene trios AY403218.1 GI:39759201 GSS:' Direct Submission Science 302 (5652), 1960-1963 (2003) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens Hominidae; Homo. Homo sapiens (human) 14671302 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /gene="STEAP" /locus_tag="HCM1484" Location/Qualifiers .1050 .>1050 99.8**%**; Score 1015.4; DB 10; Length 1050; Pred. No. 1.3e-259; 0; Mismatches 1; Indels 0; 1050 bp DNA linear GSS 15-DEC VIRTUAL TRANSCRIPT, partial sequence, genomic exons and ordering West Gude Drive, GSS 15-DEC-2003

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                                                                        CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                                                                         /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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'locus_tag="HCM1484"
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                                                         Contact: Robert Strauth. 2008
Email: cgapbs-romail.nih.gov
Tissue Procurement: Kristi A. Egland, Ira Pastan
Tissue Procurement: Kristi A. Egland, Ira Pastan
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14278 row: c column: 10
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AGENCOURT 10807821 MAPCL H
mRNA sequence.
CA488012
CA488012.1 GI:24948800
EST.
                                                                                                                                                                                                              Hominidae; Homo.

1 (bases 1 to 884)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6719746"
                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Euarchontoglires; Primates; Catarrhini;
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b sapiens cDNA clone IMAGE:6719746 5',
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Pred. No. 9.9e-196;
0; Mismatches 5;
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420

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780 801 741 660 683 600 621 540 561

TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT CTTCAGCACACAGAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT CCTGTGCTTTTTGCATTTTGCACCAAACAGCCCATGCTGAATGTAATTTTGACTGCCCTTCAGAA AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA ATGGAAAGCAGAAAAGACTACAAAACCAAGAAGACTTTGGAAAATGAAGCCTAGGAGA ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAAGATTTGGAAAATGAAGCCTAGGAGA ATAGCATCTCTGACTTTTCTCTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hTERT-HME1, LNCap"
/lab_host="EMDH10B"
/clone_lib="MARCL"
/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
/note="Vector: pcMV-SPORT6; Site_1: pcMV-SPORT6; Site_1: pcMV-SPORT6; Site_2: pcMV-SPORT6; Length 884; Indels ٥, 441 360 381 300 321 240 261 201 120 141 0

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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rockville, MD 20850,
This sequence was ma
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Science 302 (5652), 1960-1963 (2003)
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Mus musculus STEAP gene,
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 GTTTCCATCACTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA
                                         TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/locus_tag="HCM1484"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodent
Sciurognathi; Muridae; Murinae; Mus.
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AK010437.1 GI:12845880
                                                                                                                                                                                                                                                Mus musculus (house mouse)
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GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT
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                                   AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
                                                                                                             GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT
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AK010437

1211 bp mRNA linear HTC 03-APR-2004 Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2410007B19 product:six transmembrane epithelial antigen of the prostate, full insert sequence.

Euteleostomi;

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000) Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636

Shibata, K., Konno, H., Ak ., Itoh, M., Aizawa, K., Akiyama, J., Nishi, K., Nagaoka, S., Kitsunai, T., Sasaki, N., C Tashiro, H., Carninci,

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                                                                                                                                                                                                                                                                                                                                               Submitted (10.000.2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, VRL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshiki,M.; Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysa (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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6 (bases 1 to 1211)
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                                                                                                                                                                                 /organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:2410007B19"
/db_xref="taxon:T0090"
/clone="2410007B19"
                                                                       /note="unnamed protein product; putative six transmembrane epithelial antigen of the prostate (MGD|MGI:1917608, GB|AK010437, evidence: BLASTN, 100%
                                                                                                                                              /clone
/codon_start=1
/proteIn_id="BAB26938.1"
/db_xref="GI:12845881"
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                                                                                                                                                                      type="ES cells"
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HLQHAWHVDAFDCFSELQHTQEFFNWRLFVKWARIISSITFLYTLLREIIYPLVTSR
EQYFYKIFILVINKVLPMVAITLLALYYLPGELAAVVQLKRGTKYKKFPPWLDRWMLA
KKQFGLLSFFFAVLHAYYSLSYPMRRSYRYKLLNWAYKQVQQNKEDAWVEHDVWRWEI
YVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTVHALVFAWNK
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/clome_lib="NIH_MGC_76" /clome_lib="NIH_MGC_76" /clome_lib="NIH_MGC_76" /clome_lib="NIH_MGC_76" /clome_lib="NIH_MGC_76" /clome_lib="NIH_MGC_76" /clome_lib="NIH_MGC_76" /clome_morgan: liver; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc); 5'-and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by pCR. This library was enriched for full-length clones and was constructed by Clonneech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library." Ouery Match Best Local Similarity 93.6%; Pred. No. 1.6e-173; Matches 777; Conservative 0; Mismatches 47; Indels 6; Gaps 5; Matches 777; Conservative 0; Mismatches 47; Indels 6; Gaps 5; Oy 186 GCACACACGGGAACTTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGC 245	cDNA Library Preparation: CLONETECH Laboratories, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCMM549 row: b column: 05 Plate: LLCMM549 row: b column: 05 High quality sequence stop: 704. FEATURES 1881 /organism="Homo sapiens" /db xref="taxon:9606" /clone="TMAGE:4710436" /clone="TMAGE:4710436" /clone="TMAGE:4710436"	KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. REPERENCE 1 (bases 1 to 881) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. NIH-MGC http://mgc.nci.nih.gov/. OURNAL Unpublished (1999) COMMENT Email: cgapbs-remail.nih.gov Email: cgapbs-remail.nih.gov Email: cgapbs-remail.nih.gov Email: cgapbs-remail.nih.gov Email: cgapbs-remail.nih.gov	6 7 8G565247 ION 602582917F1 mRNA sequenc	Qy 841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC
RESULT 7 BE875216 LOCUS DEFINITION MRNA sequence. ACCESSION KEYWORDS SOURCE ORGANISM Homo sapiens (human) ORGANISM Hominidae; Homo. AUTHORS NATIONALI (10323992 REFERENCE TITLE JOURNAL Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: DCTD/DTP/Gazdar CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be	600 TCTACTGGGCACAATACACGCATTTTTTGCCATGTTTTAGATAAGTGGATAAACTGAATTTGTATGTA	Qy 606 AAATAAAGAAGATGCCTGGATTGAGCATGATGTTTTGGAGAATGAGATTTTATGTGTCTCT 665	OY 486 GCAGTTTGGGCTTCTCAGTTTCTTTTTGCTGTACTGCAATTTATAGTCTGTCT	Oy 306 TCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACGAAAGTCTTGCCAATGGTTTC 365

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                                                                       CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAAATGG-AGATTTATGT 659
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_69"
/clone="Organ: lung; Vector: pCMV-8PORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life Technologies."
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/mol_type="mRNA"
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University of Missouri-Columbia
M616 Medical Sciences Bldg., Co
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Prather, R. S., Antoniou, E., Garverick, H.A., Green, J.A., PROBETTS, R. S., MITCH, M. F. and Youngquist, R.S.
USDA Grant NRI-2002-03476: Bovine ESTS: Focus on Female
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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Library construction (Standard Protocol): All procedures have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, Imcg of poly(A)+ RNA was annealed at c37 degrees with 10mcg of NotI-tag-dr18 oligonucleotide (GCTGCTGCGGCGCC-tag-T18) and reverse transcribed at c37 degrees with SuperScript II (Invitrogen) reverse transcribed at c37 degrees with SuperScript II of tag' represents a tissue/stage-specific ten-base sequence identifier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            selected and preovulatory; oviduct (days 0, and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placentra/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL: http://genome.rnet.missouri.edu/Bovine/Methods.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     while not registered have known Angus pedigrees going bac at least 4 generations. Samples collected: The samples consisted of the following: germinal vesicle-stage occytes; in vitro derived embryos (2-cell, morula, lastocyst and nuclear transfer blastocyst; in vivo blastocyst and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early respected and proportional control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reproduction' to RS Prather(Primary Investigator), E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, Smith and RS Youngquist. Genetic Source: Heifers for the project were purchased from Circle A Ranch, Iberia, MO (http://www.circlearanch.com/home.html). These heifers.
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/clone_lib="bmix"
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                              http://image.llnl.gov
Plate: LLCM1713 row: h column:
High quality sequence stop: 750.
                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae; Homo.
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/tissue_type="melianotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone lib="MIH MGC_49"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
ECCRI; cDNA made by oligo-dT priming. DIrectionally cloned
into EccRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                      clone="IMAGE:4858820"
                                                                                                                                                                                                                            organism="Homo sapiens"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                    Homo
                                            796 k
BG182296 796 RAGE Library
RST1161 Athereys RAGE Library
BG182296
BG182296.1 GI:13703983
EST.
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                         sapiens (human)
sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. | "
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; Pred. No. 7e-1:
0; Mismatches
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No. 7e-155;
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У Ното
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cDNA, mRNA sequence.
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                 AGAAAGCAGTTTGGGCTTCTCAGTTTGTTTTTTGCTGTACTGCATGNCATTTATACTCTG
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Query Match 60.1%;
Best Local Similarity 97.2%;
Matches 632; Conservative
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1 (bases 1 to 796)

1 (cain, J. J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K. Offenbacher, J., Danzig, J. and Ducar, M. Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
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High quality sequence stop: Location/Qualifiers
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GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA
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216 431 9900
216 361 9596
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/clone lib="Athersys RAGE Library"
/clone lib="Athersys RAGE Library"
/clone lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 8.3e-152;
0; Mismatches 17;
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Email: cgapbs r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA446381 720 bp mRNA 1
UI-H-ED1-axr-o-23-0-UI.s1 NCI_CGAP_ED1 Homo
UI-H-ED1-axr-o-23-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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CA446381.1
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1 (bases 1 to 720)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                         /clone_lib="NCI_CGAP_ED1"
/clone_lib="NCI_CGAP_ED1"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site_1: RooR I;
Site_2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line CS5. The library was constructed according to
Bonaldo, Lemnon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonuclectide used to prime the synthesis of
firsts-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCAAGGCT.
TAG_LIB=UI-H-ED1
TAG_SEQ=CGTCAAGGCT"
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B_(Life_Technologies)"
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/db_xref="taxon:9606"
/clone="UI-H-ED1-axr-o-23-0-UI"
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                                                                                                 59.5%;
                                                                                0
                                                                              Score 605.4; DB 6;
Pred. No. 3.3e-150;
0; Mismatches 1;
                                                                                                                      Length
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Tomarev,S.I., Wistow,G., Raymond,V., Dubois,S. and Mal Gene expression profile of the human trabecular meshwo sequence tag analysis
Invest. Ophthalmol. Vis. Sci. 44 (6), 2588-2596 (2003)
                                                                                                                                                            Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
                                                         Email: graeme@helix.nih.gov
Plate: 24 row: h column:
Seq primer: M13RP1_reverse |
                                                                                                                        Tel: 301 402 3452 Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                              Contact: Wistow G
                                                                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.
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                     1. .609
                                      Location/Qualifiers
  /organism="Homo
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                                                               (ABI).
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Matches 609; Conserv
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/dev_gtage="Adult"
/lab_host="EMDH10B"
/lab_host="EMDH10B"
/clone_lib="Human Trabecular meshwork cDNA: hohphq"
/clone_lib="Human Trabecular meshwork cDNA: hohphq"
/note="Organ: Eye; Vector: pSPORT1; The cDNA,
directionally cloned in the pSPORT1 vector (Life
Technologies, Rockville, MD), was constructed at Bioserve
Biotechnology (Laurel, MD) was constructed at Bioserve
Biotechnology (Laurel, MD) essentially following the
protocols of the SuperScript plasmid System full details
of which are contained in the manufacturer's Instruction
manual (http://www.lifetech.com/). Sublibraries
(designated ho, hp, and hq) were made from the first three
35-uL fractions of cDNA from a Sephacryl S-500 HR resin
column. EST analysis was performed on the unamplified
library at the NIH Intramural Sequencing Center(NISC)."
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/db_xref="taxon:9606"
/clone="ho24h02"
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Pred. No. 3e-148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bource
                                                                                                                                                                                                                                                                                                                                                                                        Match . 58.8%; Score 598; DB 8; Local Similarity 100.0%; Pred. No. 3.1e-148;
                                         181
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High Throughput cDNA Cloning
OriGene Technologies, Inc. ( www.origene.com |
6 Taft Court, Suite 100, Rockville, MD 20850,
Tel: 301 340 3188
Fax: 301 340 8606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This EST submission is part of an on-going human full-length cloning project at OriGene Technologies, Inc. Please contact OriGene for access. OriGene Technologies, Inc. OriGene Technologies, Inc. 6 Taft Ct. Suite 100 Rockville, MD 20850 Tel: (301) 340-3188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang,X., Jay,G. and He,W.
High-throughput cloning of full-length human cDNAs directly from
---- '' ''' ontimized for large and rare transcripts
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Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Lliu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA libraries optimized 
Unpublished (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Technologies Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.origene.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.
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                                                                                    CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA
                          CTTCAGCACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT
                                                                                                                                                                                AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGCCAGCATGCTAAAAAGA
                                                                                                                                                                                                                              AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Clone_Tile_Best cancer"
/tissue_type="Breast cancer tissue, large insert, pCMV
/clone_Tib="Human breast cancer tissue, votation optimized ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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/clone="TC115356"
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RESULT 14
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                              724;
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTD/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9684 row: k column: 10
High quality sequence stop: 732.
Location/Qualifiers
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BE881257
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601492338F1 NIH_MGC_69 Homo
mRNA sequence.
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National Institutes of Health, Mammalian
Unpublished (1999)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 920)
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                                Conservative
                                                                                                     /clone="IMAGE:3894657"
/tissue_type="large_cell carcinoma, undifferentiated"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH_MGC_69"
/clone_Tib="NIH_MGC_69"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.1 kb. Library constructed by Technologies."
                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                           58.8%;
                              0,
                            Score 597.8; DB 2;
Pred. No. 3.7e-148;
0; Mismatches 37;
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AGENCOURT 41384224 NIH_MGC_278 Homo
IMAGE:7772991 3', mRNA sequence.
 Contact: Daniela S. Gerhard, Ph
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20
                                                                             Hominidae; Homo.
1 (bases 1 to 742)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, 1
                                                              Unpublished (1999)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Tissue Procurement: Meri Firpo
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM15916 row: h column: 13
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                                           GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
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                                                                                                                    TCCCGTCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pluripotent cell line derived from blastocyst inner cell mass"
/lab_host="PHIDB TonA"
/clone_lib="NHI MGC_278"
/clone_lib="NHI MGC_278"
/clone_lib="NHI MGC_278"
/clone_lib="NHI MGC_278"
/note="Organ: Blastocyst; Vector: pExpress-1; Site_1:
ECORV; Site_2: NotI; RNA obtained from pluripotent cell
line derived from blastocyst inner cell mass (cell line
HSF-1.14, NIH Registry designation UCO1. Positive for OCT4
expression by rtPCR, positive for SSEA-3, SSEA-4,
Tra-1-80 by immunofluorescence. Negative for
SSEA-1 by immunofluorescence. Passage 35. This line is a
subclone of the parental line; the parental line was
subcloned to remove aneuploid cells). cDNA was primed
using oligo-dT primer:
subcloned to remove aneuploid cells). cDNA was primed
using oligo-dT primer:
spacTAGTTCTAGATCGCGACCGCCCC(T)25-3' and cloned into
the ECORV/NotI sites of pExpress-1. Size-selection >1.25
kb resulted in an average insert size of 1.9 kb. This
primary is NIH MGC_279) and was constructed by Express
Genomics (Frederick, MD). Note: this is a Mammalian Gene
Collection library."
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 596; DB 8; Length 742;
Pred. No. 1.1e-147;
0; Mismatches 15; Indels
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421

Дb	Ş	DЬ	Ş	DЪ	Ş	Db
723 CAACAAAATGAAGAAGC 742	601 CAACAAAATAAAGAAGATGC 620	663 TCTTACGCAATGATGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 722	541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600	603 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCA	481 AGAAAGCAGTTTGGGCTTCTGAGTTTCTTTTTTGCTGTACTGCAATGCAATTTATAGTCTG 540	

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